

TITLE: MOSAIC INFECTIOUS BURSAL  
DISEASE VIRUS VACCINES  
Inventor: Boot et al.  
Serial No.: 10/046,671  
Docket No.: 2183-5238US

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**Fig.2a Alignment of IBV A-segment cDNA sequences**

Consensus	GGATACGATC GGTCTGACCC CGGGGAGTC ACCGGGGAC AGCTGACAA GGTCTGTTC CAGATGCAA CTCT	75
CEP94-A	.....G.T... ..T.....	75
D6948-A	.....T.A... ..C.....	75
TY89-A	.....	
Consensus	CCTTCTACAA TGTATCTTT GATGTTTAT AGAGATCAGA CAAAGATCG CAGGCTGAC TAACTGCAA GATCA	150
CEP94-A	.....C..... ..C..... ..A.....	150
D6948-A	.....T..... ..F..... ..G.....	150
TY89-A	.....	
Consensus	AACCCACAG ATTGTTCCCT TCATAGGAG CCTTCTGATG CCAACACCG GACCGGGTC CATTCGGAC GACAC	225
CEP94-A	.....	225
D6948-A	.....	225
TY89-A	.....	
Consensus	CCTGAGGAG CACACTCTCA GGTCTGAGAC CTGACCTAC AATTGACTG TGGGGACAC AGGCTCAGG CTAT	300
CEP94-A	...G.....	300
D6948-A	...A.....	300
TY89-A	.....	
Consensus	TGTCTTTTC CCTGGTTCC CTGCTCAAT TGTGGTGCT CACTACACAC TGCAGGCAA TGGAACTAC AAGTT	375
CEP94-A	.....A.....	375
D6948-A	.....T.....	375
TY89-A	.....	
Consensus	CGATCAGAT CTCTGACTG CCGAAGACT ACCGGCCAGY TACACTACT GCAGCTAGT GATCGAGT CTGAC	450
CEP94-A	.....T.....	450
D6948-A	.....C.....	450
TY89-A	.....	
Consensus	AGTGAAGTCA AGCACTTC CTGGTGGCT TTATGCACTA AATGGACCA TAAAGCCCT GACCTTCCAA GGAG	525
CEP94-A	.....T..... ..C.....	525
D6948-A	.....C..... ..T.....	525
TY89-A	.....	
Consensus	CCTGAGTGA CTGACGATG TTGCTACAA TGGGTGATG TGTGACAGG CCAACATCA GACAAATY GGGAA	600
CEP94-A	.....T.....	600
D6948-A	.....C.....	600
TY89-A	.....	
Consensus	GCTCTAGTA GGGGAAGGG TACGCTCTT CAGCTTACC ACATCATAT ATCTTGGTA TGTGAGCTY GGTGA	675
CEP94-A	.....C..... ..G..T.....	675
D6948-A	.....A..... ..A..C.....	675
TY89-A	.....	
Consensus	CCCATTCCT GCGATAGGC TTGACCCAA AATGATGAC ACATGTGACA GCAGTGACAG GCCAGAGTC TACAC	750
CEP94-A	.....A..... ..T..... ..C.....	750
D6948-A	.....T..... ..C..... ..A.....	750
TY89-A	.....	
Consensus	CATACTOCA GCGATGATT ACCAATCTC ATCAGAGTAC CAACGAGTG GGTATACAT CCACTGTTC TCAGC	825
CEP94-A	.....C.....	825
D6948-A	.....G.....	825
TY89-A	.....	
Consensus	YAAATATGAT GGCATACAA GCTCAGCT TGGGGAGAR CTCGTGTTT AAACAAGCT CCAGGCTT RTACT	900
CEP94-A	C..C..T... ..G..T... ..G..... ..C..... ..G.....	900
D6948-A	T..T..C... ..A..C... ..A..... ..A..... ..A.....	900
TY89-A	.....	
Consensus	GGTGTCTACC ATCTACTTA TAGCTTTGA TGGGACGCG GTAAATACCA GAGCTGTGC GGCACACT GGGCT	975
CEP94-A	...C..C... ..C..... ..A..... ..G..... ..A.....	975
D6948-A	...T..T... ..T..... ..T..... ..A..... ..G.....	975
TY89-A	.....	

[illegible]

Fig. 2a Contd.										
Consensus	RACGACCGGC	ACTGACACCC	TTCGCCATT	CAATTTTGTG	ATTCCACGCA	RCAGATGAMC	GACGGCATC	ACATC		1050
CEP94-A	G...A....	. .C.....	. .T.....	...C....	.....A..	A.....	.....	.....	1050	
D6948-A	A...G....	. .T.....	. .A.....	...A....	.....C..	G.....	.....	.....	1050	
TY89-A	-----	-----	-----	-----	-----	-----	-----	-----		
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Consensus	CATCAAAGTG	GAGATAGTGA	CCTCCAAAG	TGGTGCTCMG	GCGGGGATC	AGAATGCTTG	GTCCGCAAGW	GGGAG		1125
CEP94-A	.....	.....	.....	. ....	. .A....	.....G..	. .G....A	.....	1125	
D6948-A	.....	.....	.....	.....	. .G....	.....A..	. .A....T	.....	1125	
TY89-A	-----	-----	-----	-----	-----	-----	-----	-----		
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Consensus	CCTAGCATMG	ACGATCCATG	GTGGCACTA	TCCMGGGCC	CTCCGTCODG	TCACCTTAGT	BGCTTAGGAA	AGAGT		1200
CEP94-A	.....	.....T..	.....	.....	.....	...G....	G.....	.....	1200	
D6948-A	.....	.....C..	.....	.....	.....	...A....	A.....	.....	1200	
TY89-A	-----	-----	-----	-----	-----	-----	-----	-----		
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Consensus	GGCACACGGA	TCTGTGTTTA	CAGTGCCTG	GGTGACCAAC	TTCGAGCTGA	TCCCAATCC	TGACTAGCA	AAGAA		1275
CEP94-A	.....	. .C.....	.....T..	.....	.....	.....	.....	.....	1275	
D6948-A	.....	. .T.....	.....C..	.....	.....	.....	.....	.....	1275	
TY89-A	-----	-----	-----	-----	-----	-----	-----	-----		
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Consensus	CCTGTGTACA	GAATACGGCC	GATTGACCC	AGAGCCATG	AACTACACAA	AATTGATACT	GAOTGAGAGG	GAACC		1350
CEP94-A	.....T..	.....	.....	.....	.....	.....	.....	.....	1350	
D6948-A	.....C..	.....	.....	.....	.....	.....	.....	.....	1350	
TY89-A	-----	-----	-----	-----	-----	-----	-----	-----		
<hr/>										
Consensus	TCTTGCCATC	AAGACCTGTT	GGCCAACAG	GGGTACACT	GACTTTGTG	ATTACTIONT	GGGTGAGGCC	GAOCT		1425
CEP94-A	.....	.....C..	.....	.....	.....T..	. .A....	.....	.....	1425	
D6948-A	.....	.....A..	.....	.....	.....C..	. .G....	.....	.....	1425	
TY89-A	-----	-----	-----	-----	-----	-----	-----	-----		
<hr/>										
Consensus	CAACTCTCCC	CTGAGATTG	CAGGCGATT	TGGCTTCAA	GACATATCC	GGCCCHTAG	GAGGATAGCT	GTGCC		1500
CEP94-A	.....	.....	.....	C.....	.....	...A....	.....	.....	1500	
D6948-A	.....	.....	.....	T.....	.....	...C....	.....	.....	1500	
TY89-A	-----	-----	-----	-----	-----	-----	-----	-----		
<hr/>										
Consensus	GGTGGTCTCT	ACATTGTTCC	CACCTGCGGC	TCCCCYAGCC	CATCGANTTG	GGGANGTOT	AGACTACCTG	CTGGG		1575
CEP94-A	.....C..	. .T.....	...T....	.....	.....	.....	.....	.....	1575	
D6948-A	.....T..	. .C.....	...C....	.....	.....	.....	.....	.....	1575	
TY89-A	-----	-----	-----	-----	-----	-----	-----	-----		
<hr/>										
Consensus	CGATGAGCCA	CAGGCTGCTT	CAGGACTGC	TGAGCCCGG	TCAGGAAAAG	CAAGAGCTGC	CTCAGGCCCG	ATAGG		1650
CEP94-A	.....	.....	.....	.....	.....	.....	.....	.....	1650	
D6948-A	.....	.....	.....	.....	.....	.....	.....	.....	1650	
TY89-A	-----	-----	-----	-----	-----	-----	-----	-----		
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Consensus	GCNGCTACT	CTGGCGCCG	ACAGGGGTA	CGAGGTATC	GGGATCTTT	TTCAGGTGCC	CCGAGATCTT	GTAGT		1725
CEP94-A	...G....	.....	.....	.....	...A....	. .C....	.....C..	.....	1725	
D6948-A	...A....	.....	.....	.....	...G....	. .T....	...T....	.....	1725	
TY89-A	-----	-----	-----	-----	-----	-----	-----	-----		
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Consensus	CGAGGGGATT	CTTGCTTCA	CTGGGTACT	CCGGGGTCA	CACAACTCG	ACTGGGTGTT	BAGAGAGGTT	GCCAC		1800
CEP94-A	.....T..	.....G..	...T....	.....	.....	.....	A.....	.....	1800	

Fig. 2a Contd.										
Consensus	RACGACCGGC	ACTGACACCC	TTTGGCATT	CAATTCTTGT	ATTCCACCA	CGAGATGAC	CCAGCCCATC	ACATC		1050
CEP94-A	G...A....	..C.....	..T.....	...C....	.....A..	A.....	.....	.....	1050	
D6948-A	A...G....	..T.....	..A.....	...A....	.....C..	G.....	.....	.....	1050	
TY89-A	.....	.....	.....	.....	.....	.....	.....	.....		
Consensus	CATCAAACTG	GAGATAGTGA	CCTCCAAAAG	TGGTGGTCAG	GCGGGGATC	AGATGTCGTG	GTCCGCAAGG	GGGAG	1125	
CEP94-A	.....	.....	.....	..A.....	..A.....	.....G..	...G...A	.....	1125	
D6948-A	.....	.....	.....	..G.....	.....A..	.....A..	..A...T	.....	1125	
TY89-A	.....	.....	.....	.....	.....	.....	.....	.....		
Consensus	CCTAGCATTG	ACGATCCATG	GTGGCACTA	TCCAGGGGCC	CTCCGTCGGG	TCACCTCATG	AGCTTACGAA	AGAGT	1200	
CEP94-A	.....	.....T..	.....	.....	.....	...G...	G.....	.....	1200	
D6948-A	.....	.....C..	.....	.....	.....	...A...	A.....	.....	1200	
TY89-A	.....	.....	.....	.....	.....	.....	.....	.....		
Consensus	GGCAACAGGA	TCCTGTGTTA	CGGTGCTGAG	GGTGACCAAC	TTGAGCTGA	TCCCAATCC	TGACTAGCA	AAGAA	1275	
CEP94-A	.....	..C.....	.....T..	.....	.....	.....	.....	.....	1275	
D6948-A	.....	..T.....	.....C..	.....	.....	.....	.....	.....	1275	
TY89-A	.....	.....	.....	.....	.....	.....	.....	.....		
Consensus	CCTGGTACAA	GAATACGGCC	GATTGACCC	AGAGCCATG	AATACACAA	AATTGATCT	GAATGAGAGG	GAAGG	1350	
CEP94-A	.....	.....T..	.....	.....	.....	.....	.....	.....	1350	
D6948-A	.....	.....C..	.....	.....	.....	.....	.....	.....	1350	
TY89-A	.....	.....	.....	.....	.....	.....	.....	.....		
Consensus	TCCTGGCATC	AAGACCTGTT	GGCAACAGG	GGGTACACT	GACTTTGGTG	ATGACTTCAT	GGGGTGAGCC	GAAGT	1425	
CEP94-A	.....	.....C..	.....	.....	.....T..	..A.....	.....	.....	1425	
D6948-A	.....	.....A..	.....	.....	.....C..	..G.....	.....	.....	1425	
TY89-A	.....	.....	.....	.....	.....	.....	.....	.....		
Consensus	CAACTCTGCC	CTGAGATTG	CAGGCGATT	TGGCTTCAA	GACATATCC	GGCCGATAG	GAGGATAGCT	GTGCC	1500	
CEP94-A	.....	.....	.....	.....	.....	.....A...	.....	.....	1500	
D6948-A	.....	.....	.....	.....	.....	.....C..	.....	.....	1500	
TY89-A	.....	.....	.....	.....	.....	.....	.....	.....		
Consensus	GGTGGTCTCT	ACATTGTTCC	CACCTGCGGC	TCCCTTAGGC	CATCGAATTG	GGGAGGTGT	AGACTACCTG	CTGGG	1575	
CEP94-A	.....C..	..T.....	.....T..	.....	.....	.....	.....	.....	1575	
D6948-A	.....T..	..C.....	.....C..	.....	.....	.....	.....	.....	1575	
TY89-A	.....	.....	.....	.....	.....	.....	.....	.....		
Consensus	CGATGAGGCA	CAGGCTGCTT	CAGGACTGC	TGAGCCGCG	TCAGGAAAG	CAAGACTGC	CTCAGGCCGC	ATAGG	1650	
CEP94-A	.....	.....	.....	.....	.....	.....	.....	.....	1650	
D6948-A	.....	.....	.....	.....	.....	.....	.....	.....	1650	
TY89-A	.....	.....	.....	.....	.....	.....	.....	.....		
Consensus	GCGCTACTCT	CTGCGCGCG	ACAGGGGTA	CGAGGTATC	GGGATCTCT	TTGAGGTGCC	CCGAGATCTT	GTAGT	1725	
CEP94-A	.....G..	.....	.....	.....	.....A..	..C.....	.....C..	.....	1725	
D6948-A	.....A..	.....	.....	.....	.....G..	..T.....	.....T..	.....	1725	
TY89-A	.....	.....	.....	.....	.....	.....	.....	.....		
Consensus	CGAGGGGATT	CTTCTTCAC	CTGGGTACT	CCGGGGTCA	CACAACTCG	ACTCGGTGTT	AGAGAGGGTT	GCCAC	1800	
CEP94-A	.....	..T.....	.....G..	.....T..	.....	.....	A.....	.....	1800	
D6948-A	.....	..C.....	.....A..	.....C..	.....	.....	G.....	.....	1800	
TY89-A	.....	.....	.....	.....	.....	.....	.....	.....		
Consensus	GCTATTCCCT									

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Fig.2a Contd. Alignment of IBV A-segment cDNA sequences

Consensus	AGTCATGGA TATGCTCCAG ATGGGTTACT TCCACGGAG ACTGGGAGAG ATTACACCGT KGTCCACATA GAGA	2025
CEP94-A	.....C.....T.....	2025
D6948-A	.....T.....G.....	2025
TY89-A	.....	
Consensus	TGTCTGGAC GACGACATTA TGTCTGCA AGATCCATA CCTCTATTG TGGGAAACAG TGGAAATCA GCCAT	2100
CEP94-A	.....T.....T.....T.....	2100
D6948-A	.....C.....C.....	2100
TY89-A	.....	
Consensus	AGCTTACATG GATGTGTTTC GACCCAAAGT CCGATCCAT GTGGCTATGA CCGGAGCCCT CAACTCTTCT GCGCA	2175
CEP94-A	.....A.....T.....T.....T.....	2175
D6948-A	.....C.....C.....C.....C.....	2175
TY89-A	.....	
Consensus	GATTGAGAA GTTAGCTTTA GAGGACCA GCTGCTACT GCACACGAC TTGGCTTAA GTTGCTGCTT CCGG	2250
CEP94-A	.....A.....T.....T.....	2250
D6948-A	.....C.....C.....C.....	2250
TY89-A	.....	
Consensus	WCATTTGAY GTTAACACCG GTTCCACTG GGCACGCTT ATCAACGCTT TTTCTACAA TCGCGGAC TCGA	2325
CEP94-A	A.....C..T..A.....C.....A.....C.....	2325
D6948-A	T.....T..C..G.....T.....G.....T.....	2325
TY89-A	.....C.....C.....A.....	29
Consensus	CAGGTTWCT TACCTCAACC TWCCTATCT TCCACCAAW GCGGAGCTC AGTWCATCT KGCCTTGGH GCCTC	2400
CEP94-A	...C..C..C.....A..A..C..T...C..AT..A.....C...A..C..C..T...A...T..A..	2400
D6948-A	...C..C..T.....T..A..C..T...C..AT..A.....C...A..G..C..G...A...C..T..	2400
TY89-A	...T..A..C.....T..C..T..C...A..CA..T...T...T..C..T..G...C...A...C..	104
Consensus	WGATTCAAA GAGACCCGAG AACGCGARR TCTCTGSGW GCMATGAGG CWCWCGMA CCGGACCCA YRTT	2475
CEP94-A	A.....C.....GAG T..C..CA..A..A.....A..A..A..C...G.....C..A..	2475
D6948-A	A.....C.....GAG C..C..CA..A..C.....A..A..A..C...G.....C..G..	2475
TY89-A	C.....A.....AGA C..T..GC..T..A.....C..T..T..A...C.....T..G..	179
Consensus	CCCTGCGC CTGCTGCT TCTGTGCTT GGAAGAAAY GGAATGTA CYGATATGC YAACTGCGH CTCAG	2550
CEP94-A	..AA..T..A...AGT..G.....C.....G..T.....G..T..C.....C.....A.....	2550
D6948-A	..AA..T..G...AGC..G.....C.....G..T.....G..T..T.....C.....A.....	2550
TY89-A	..GC..A..T...CAG..C.....T.....A..C.....A..C..C.....T.....C.....	254
Consensus	CGACCCGAC GGCATGGA TGGGAAAT TCTGCAAY GCGGCGAG CCGGAGCA GTGCGAGG GCGA	2625
CEP94-A	.....C..TC.....CGA.....T..T.....C..A..A..A..A..C.....A..G.....	2625
D6948-A	.....C..TC.....CGC.....T..C.....C..A..A..A..A..C.....A..A.....	2625
TY89-A	.....A..CA.....AAA.....C..A.....T..T..C..G..C..A.....G..G.....	329
Consensus	GTATGGACR GCGGCTACG GATGGAGGC TGGGGCCCC ACCCGGAGG AGGCACAGG GGAAGAAGC ACAGC	2700
CEP94-A	...C..G..A..A.....TC..G.....A.....G..A.....A.....A.....	2700
D6948-A	...C..G..A..A.....CC..G.....T.....G..A.....A.....A.....	2700
TY89-A	...T..C..G..T.....TA..A.....G.....A..G.....G.....G.....	404
Consensus	GATCTGAG AGATGARA CATGGGCAT CTACTTGA ACACCGAAT GGTAGCACT CAATGGCAC CCGG	2775
CEP94-A	.....A.....G..C.....T.....A.....T.....A.....	2775
D6948-A	.....A.....T.....T.....A.....T.....G.....	2775
TY89-A	.....C.....A..G.....C.....G.....C.....A.....	679
Consensus	GGCAGCCCC GCGGCTTGA AGTACTGCA RAACACAGG GAAATACCG ARCCGACGA GCACTATCTA GACTA	2850
CEP94-A	G.....A.....G.....C.....G..C..A.....T..T.....	2850
D6948-A	G.....G.....G.....C.....T..T..A.....C..T.....	2850
TY89-A	C.....C.....A.....A.....A..C.....C..C.....	554
Consensus	YGTCAATGR GAGAAGGCC GGTGGGCTC AGAGAACAR RTCTTAAGG CAGCTACGC GATCTACGG GCTCC	2925
CEP94-A	C.....T..A.....A.....A..A..C.....T.....	2925
D6948-A	C.....T..A.....A.....A..A..C.....T.....	2925
TY89-A	T.....C..G.....G..T.....C.....	629

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Fig.2a Contd. Alignment of IEDV A-segment cDNA sequences

Consensus	AGGACAGGCG GAGCCACCCC AAGCTTTCAT MGACGAAGTY GGCATGCTCT ATGAAATCAA CCATGCGCGT GGTCC	3000
CEP94-A	.....A..G.....T.....T....AA.....A...C..	3000
D6948-A	.....A..G.....C.....C....AA.....G...C..	3000
TY89-A	.....T..A.....C.....C....GG.....G...T..	784
Consensus	MAACCAAGAG CAGATGAAG ATCTGCTCTT GACTGCGATG GAGATGAAGC ATGCAATCC CAGCGCGCT CTACC	3075
CEP94-A	A.....A..A.....A..T.....T.....T...T...	3075
D6948-A	C.....A..A.....A..T.....C.....C...C...	3075
TY89-A	A.....G..G.....G..C.....C.....C...C...	779
Consensus	AAAGCCGAG CCAAAACCCA ATGCTCCMC ACAGAGCCC CCGGCGGC TGGGCGCTG GATCAGGCG GTCCT	3150
CEP94-A	.....C.....A.....T.....T.....A.C.....	3150
D6948-A	.....C.....A.....T.....T.....G.F.....	3150
TY89-A	.....A.....T.....A.....A.....A.G.....	854
Consensus	TGATGAGGAC YTGAGTGAG GTWCTGGGA GTCTCCGAC ACCACCGCG CAGGTGTGA CACCAATTG KBBT	3225
CEP94-A	...T.....C.T.....TA.....T.....CG GACT.	3225
D6948-A	...T.....C.T.....CT.....C.....CG GCGA.	3225
TY89-A	...C.....T.G.....CT.....T.....AA TCAC.	929
Consensus	AGGAGATTC AAATTGGATC CTTGCGCGG TCCCC	3260
CEP94-A	.CAC..C.C.....	3260
D6948-A	.CAC..C.C.....	3260
TY89-A	.GTG...T.G.....	964

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<b>Fig.2b</b>	<b>Alignment of IBDV B-segment cDNA sequences</b>	
Consensus	GGATACGATG GGTCTGACCC TCTGGAGTC ACCTAATTAAC GTGGCTACTA GGGGTGATTA CCGGGGCTGG CTGCC	75
CEP94-B	.....C...AA ..G.....G. ....	75
D6948-B	.....T...GC ..A.....A. ....	75
Consensus	ACGTTAGTGG CTCTCTTCT TGTATGTTCT ECGACCAAGA GTGACTTTT CAATAGTCCA CAGGGGCGAA GCAGG	150
CEP94-B	.....G..... ..A..... ..C..... ..C. ....	150
D6948-B	.....A..... ..G..... ..T..... ..A. ....	150
Consensus	ATHTCAGCAG GGTTCGGCAT AAGGCTTACH GCTGACGAGS AYGTGGAGGA ACTCTTGATC CCTGAGTTT GGGTG	225
CEP94-B	..C..... ..T..... ..A. ..C..... ..T..... ..A..T. ....	225
D6948-B	..A..... ..A..... ..G. ..T..... ..C..... ..G..C. ....	225
Consensus	CCACCTGAGG ATCCCTTTC CAGCCTTMT CAGCTGCGCA AGTTCTCTAG GGAATACGCG TACAATTTT TGCGS	300
CEP94-B	.....GC..T. .... ..A..... ..A..... ..A..G..... ..AG..T. ....	300
D6948-B	.....CT..G. .... ..T..... ..C..... ..G..A..... ..GA..C. ....	300
Consensus	CCACGCTTC TCCCTGAGAA TGAGGATAT GAGACGAGTC AATTAATCCC GAGCTGAGCA TGAGTGGGTC AGGTA	375
CEP94-B	.....G..C..... ..C..... ..A...T..... ..C.A. ....	375
D6948-B	.....A..T..... ..T..... ..T...C..... ..A..G. ....	375
Consensus	GAGGGGCTG TTATAAACC NACTCTACT CTCCCTATG GAGATCAGA GTACTTCGCA AAREACTACC CAACA	450
CEP94-B	..A..G.... ..C..T..... ..T..... ..T..... ..A..G..... ..G.....	450
D6948-B	..G..A.... ..A..C..... ..C..... ..C..... ..T..... ..A.....	450
Consensus	CATGGGCTCA GCAAGGAGAA GCGCAATGCG TACCCGCGCG AYATGCAAT ACTCAGCAGS ATGTTTACT TTTT	525
CEP94-B	..T.....T. ....G.. ..A..... ..C..... ..C..... ..T...C. ....	525
D6948-B	..C.....G. ....A..... ..C..... ..T..... ..T..... ..C...T. ....	525
Consensus	CTCCGCTTC CAGAGGCGCA GGAATGCTT AAGATGAGG TACGCTTMT TACCCAAAC ATGAGGAGTA AGGCC	600
CEP94-B	.....A.....A ..C..GG..A ..G.....A ..A.....CT. G..... ..A..G..C. ..G....	600
D6948-B	.....C.....C ..A..TAA..T ..A.....G. ..C.....AC. A..... ..T..A..T. ..A....	600
Consensus	TATGAGATG GAGCTTACT GAGACAGGCA ACCTGACTTG TGCTATGAA GAGGCTTGGC ACTGAGAGAA ACCCA	675
CEP94-B	..T..A.... ..A..A ..TC..... ..G..C..... ..G.....C..... ..A.....	675
D6948-B	..C..G.... ..G..C ..CA..... ..T..T..... ..A.....T..... ..G.....	675
Consensus	AACAGATC CTCTAAGCT TGGTACACT TTGAGAGCA TGGGCGACT ACTTGACATC AACTACCGG TAGGC	750
CEP94-B	.....G..... ..T..... ..C..G..... ..AC..... ..G.....	750
D6948-B	.....A..... ..C..... ..A..C..... ..T..... ..G.....	750
Consensus	CCACCGGCTG AGGATGACAA GCGCTGGTTC CCACTACAA GGTGGGCTTC AAGGATGTTG GTACGAGCG GAGAC	825
CEP94-B	.....G..... ..A..... ..C..... ..A..... ..A.....	825
D6948-B	.....A..... ..G..... ..A..... ..T..... ..C.....	825
Consensus	GTAGATGGG AMTTGAGGT TGAGATAC CTGCCAATA TCACCTCAA GTCATCAAT GACTTCGCT ATGTV	900
CEP94-B	.....C..C..... ..A..T..... ..A..... ..A..A..... ..A.....	900
D6948-B	.....G..A..... ..G..C..... ..A..... ..G..C..... ..T.....	900
Consensus	GCTGGACCA AAGGAGAAC GATGGGAGS ATGATAGCTA TTTTCAACA GTTCTTCTTA GAGCTATCA CACTG	975
CEP94-B	.....G..A..... ..C..... ..T..... ..C..A..... ..CA..... ..A.....	975
D6948-B	.....A..... ..T..... ..C..... ..A..G..... ..TC..... ..G.....	975
Consensus	YTGAGCAGS GTCCAGGAC AAAGGCTCA AACAGAGGA AGCTCTCAG CATGTTAAT GACTATGCT ACTTA	1050
CEP94-B	T.....A..... ..G..... ..A..... ..G..... ..T..... ..T.....	1050
D6948-B	C.....G..... ..A..... ..G..... ..G..... ..C..... ..C.....	1050
Consensus	TGATGCTGC TTGTGTTTC NAGGCTGAG AGGTACGACA AAGTACATG GCTACCAAG ACCCGGACA TATGG	1125
CEP94-B	.....C..... ..A..... ..A..... ..T..... ..G..... ..G.....	1125
D6948-B	.....T..... ..C..... ..G..... ..C..... ..T..... ..T.....	1125
Consensus	TGACTCCAT CCGCAACACA CCTCATGATC TGTATGATGA CTTGGGCGGT GATGTGCAAT AGCCCAATTA AGCTG	1200
CEP94-B	.....C..... ..T..... ..C..... ..C..... ..C..... ..T.....	1200
D6948-B	.....A..... ..A..... ..A..... ..T..... ..C..... ..C.....	1200

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Fig.2b Contd. Alignment of IBV B-segment cDNA sequences

Consensus	TTGACATTG	ARGGGTGTCC	RTCACTCTAC	AARTCAACC	CGTTAGAGG	WGGGTTAAC	AGGTCCTTG	AGTGG	1275
CEP94-B	.....	A.....	A.....	..A.....	...C.....	A...T.G...	.....C.....	.....	1275
D6948-B	.....	G.....	G.....	..G.....	...T.....	T...C.A...	.....G.....	.....	1275
Consensus	ATATGCTC	CGGAGAAC	CAGGCTTW	GTAATCCG	ACACATATA	CATTCTTC	TGGACAGT	GGTAC	1350
CEP94-B	...T...C...	...A.....	...TC.T...	...G.....	.....C...	..A.....	.....	.....	1350
D6948-B	...A...T...	...T.....	...CT.A...	...T.....	.....T...	..C.....	.....	.....	1350
Consensus	TCAATTGAC	TAGAGAGG	TGGGCAAC	TGCACGTC	AACATGCA	GGCGGATG	TACTACATC	TGACC	1425
CEP94-B	.....	.....	.....	...F..C...	.....A.....	.....A.....	.....A..C...	.....	1425
D6948-B	.....	.....	.....	...G..T...	.....G.....	.....C.....	.....C..T...	.....	1425
Consensus	AGAGGTGAT	CGGAYAGG	TGACCGATG	TTCATCATA	CATGGGAC	CTTTCGATG	AACATGGCC	CGGCT	1500
CEP94-B	.....G.....	..A..C.....	..C.....A...	.....A.....	.....C.....	.....C.....	.....T...	.....	1500
D6948-B	.....A.....	..C..T.....	..T.....C...	.....G.....	.....G.....	.....G.....	.....A...	.....	1500
Consensus	CTAGTGTG	ACTATCTG	TCTGATATG	AGCTTCATA	TGAGACATA	TGGTCAAGC	AGTGGGATG	CAGCC	1575
CEP94-B	.....G.....	.....G..C.....	..A.....A...	...G..A..T.....	.....C.....	.....C.....	.....	.....	1575
D6948-B	.....T.....	.....A..T.....	..T.....T...	...T..G..C.....	.....A.....	.....T.....	.....	.....	1575
Consensus	ACCTTCACA	ACAACCACT	TTTACGAC	CTGTCTTG	ACCATGGAA	CTTGATGAT	CAGCTAGAC	CAGAC	1650
CEP94-B	..G.....	.....C..CT.G...	..G..A.....T...	.....C.....GA	..G..C..A.....	.....	.....	.....	1650
D6948-B	..C.....	.....T..TC.T...	..C..T.....A...	.....T.....AG	..A..T..T.....	.....	.....	.....	1650
Consensus	AGCGAGAT	TCAATCAAT	TGAGACAG	CTGGATCA	ACTTAAAT	TGAGAGTCC	ATTGATATA	TGAGG	1725
CEP94-B	.....G.....	.....A.....	..G.....A..T.....	.....T.....	.....T.....	.....T.....	..C.....	.....	1725
D6948-B	.....A.....	.....G.....	..G..C.....	.....C.....	.....C.....	.....C.....	..T.....	.....	1725
Consensus	GGCAAGCTA	GACAGCTGT	CCCTCTCA	CACCAAGGT	ACCTGATGG	GGGGTTGAA	CGGAGCAAT	CGAGC	1800
CEP94-B	.....G.....	.....T.....	.....T.....	.....T.....	.....G.....T...	.....A..T...	.....A..T...	.....	1800
D6948-B	.....C.....	.....C.....	.....T.....	.....T.....	.....A.....C.....	.....G...C.....	.....	.....	1800
Consensus	CCACTGTG	AGCTGACCT	ACTGGGTGG	TGGGACAT	ACAGCAAGA	TCTTGGATC	TATGTGCGG	TGCTT	1875
CEP94-B	.....T.....	...T.....	..A..G...A..T..A...	.....C.....	.....C.....	.....C.....	.....T.....	.....	1875
D6948-B	.....A.....	.....G.....	..C..A...T..A..T...	.....T.....	.....T.....	.....T.....	.....	.....	1875
Consensus	GACAAGGAC	GCTATTTTG	TTCTGCTGG	TATCCCAAG	GATAGAGAA	TAAGAGTTC	AATCCCAAG	TGAGG	1950
CEP94-B	.....C.....	.....T.....	.....G.....	..A.....C..G..T...	..G.....A..C...	.....	.....	.....	1950
D6948-B	.....T.....	.....C.....	.....A.....	..G.....T..A..C...	..A.....G..T...	.....	.....	.....	1950
Consensus	ATGAGCAG	CATCAAGT	WTCAGAT	GAGGCTTGA	GTTGGTAGG	TGGTGGAC	TACCACTCC	TGAC	2025
CEP94-B	.....G.....	.....G..A.....T...	.....	.....	.....	.....	.....	.....	2025
D6948-B	.....A.....	.....A..T.....C...	.....	.....	.....	.....	.....	.....	2025
Consensus	AAAGCTTCA	AGAAATATC	AGTGCCTC	CGGCGCATC	TGAGGCGCA	GGGTTCCGC	CTGATGAT	TGCTT	2100
CEP94-B	.....C.....	.....T..C...G.C..C...	.....	.....	.....A.....C.....	.....A.....	.....A.....	.....	2100
D6948-B	.....T.....	.....C..T...A.T..A...	.....	.....	.....A.....G.....	.....T.....	.....C.....	.....	2100
Consensus	GGGATGAT	CGGATGTC	GGGTTGCG	GAGCTTTC	AAAGCTTCA	TATCAGCTG	ACGATACAT	CGGAG	2175
CEP94-B	.....T...C.....	..A.....T..G..C...	.....	.....	.....T.....	.....C.....T..T...	.....	.....	2175
D6948-B	.....A...T.....	..C.....A..A..T...	.....	.....	.....C.....	..A.....C..G...	.....	.....	2175
Consensus	AGCTTGGCG	AATTAACAT	GGGATGCG	CCCAAGCTC	CAATGTCAA	CAGACCAATC	AACATGCGG	GGCTT	2250
CEP94-B	.....A.....	.....G..A..G.....	.....G..C...	.....	.....	.....T..G..A..C	.....	.....	2250
D6948-B	.....C.....	.....T..G..A.....	.....A..T...	.....	.....	.....C..T..G..A	.....	.....	2250
Consensus	AGGACATCA	GCAATGCGT	CAGACCGGT	CGGTAYAGRA	ATGAGCGCG	ACTGATGAT	CTGCTCTTC	TAGCC	2325
CEP94-B	.....C.....	.....T.....	...C..G..C.....	.....G.....T...	.....T.....	.....T.....	.....	.....	2325
D6948-B	.....T.....	.....T.....C...	...T..A..T.....	.....A.....C.....	.....C.....	.....C.....	.....	.....	2325
Consensus	ACGCGGGA	GGGCTTCA	GGATGATG	AGGCGGAG	CAGAGCGGA	GAACTCCAC	AGCTTATGC	CGGAT	2400
CEP94-B	..A..AA..A...	...T..G..A..T...T...	.....	.....A.....	.....C.....	.....A..C	.....	.....	2400
D6948-B	..C..CC..C...	..A..A..G..C...C...	.....	.....G.....	.....T.....	.....C..T...	.....	.....	2400

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Fig.2b Contd. Alignment of IBV B-segment cDNA sequences

Consensus	GACCCCGATG CAGACTGCTT TGAAGTCTA GAACTCTCT CAGACTCTCT GAGAAAGCC GACCTTCCCA GCAG	2475
CEP94-B	..... C...A.A... ..T... ..T... ..C... ..	2475
D6948-B	..... T...C.G... ..C... ..G... ..T... ..	2475
Consensus	GTCCTCACT CAGACTCTT GGAACAAAC GAGCTCTTG AAGCTGTCA GTCACTTCT GTTCACTTC CAG	2550
CEP94-B	.....C... ..C... ..A..T... ..G..T..C ..T... ..C... ..	2550
D6948-B	.....T... ..T... ..G..C... ..A..C..A ..C... ..A... ..	2550
Consensus	TACCCAGAG TYAAGAACCC ACAGACGCC TCCAGCCCG TTCTTGGCT CCAGCTGCC GCGAGAGAG CCAC	2625
CEP94-B	.....A..C..... ..A..... ..A..... ..A..... ..	2625
D6948-B	.....G..T..... ..T..... ..G..... ..G..... ..	2625
Consensus	GCTCTCCAG CAGCTCTCT CAGAGCAGG AGAGCAGAC CAATGGGAT GAGACTCCA ACAGCTCCA AGAC	2700
CEP94-B	.....C..... ..A..... ..C..... ..C..... ..	2700
D6948-B	.....A..... ..G..... ..T..... ..T..... ..	2700
Consensus	GCCGTGAAA TGGCCAAAG GCGGCAAGC CAAAGAGAG GCCGCCAAT GCCATGTGG GAGCACTCA AGAG	2775
CEP94-B	.....C..... ..G..... ..C..... ..C..... ..	2775
D6948-B	.....A..... ..A..... ..T..... ..T..... ..	2775
Consensus	AGGACTAA TCCAGAGCC GTATCCCG GCTTGGCT GCGGGGCCC CC	2827
CEP94-B	.....T..... ..T..... ..T..... ..T..... ..	2827
D6948-B	.....C..... ..C..... ..C..... ..C..... ..	2827



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Fig.3a IBV polyprotein alignment

Consensus	HTMLODOTQQ IUVVIRSLIM PTGDSASPD DTLNCHTARS ETSTHMLTVQ DTGSHLIVFF PGFFGSIVGA HTILO	75
CEF94-PP	.....	75
D6948-PP	.....	75
TY89-PP	.....	
Consensus	ENGVTKPDQM LLAQHLFAS YNYCLVRSR LTVRSSTLPG GVTALSGTIR AVTFQGSLSR LTVSTINGLM ENEM	150
CEF94-PP	.....	150
D6948-PP	.....	150
TY89-PP	.....	
Consensus	INDKIGNVLV GEGVTLSLP TSTLQTVEL GDPFPAIGLD PKWATCDSS DRPVYTIYA ADOTFESQY Q.GGV	225
CEF94-PP	.....	225
D6948-PP	.....	225
TY89-PP	.....	
Consensus	TITLPSASID AITELS.GGE LWTQTSV.GL LGATITILIG PDOTAVITRA VAA.HSLT.G TDEL.FPW.V IPT.E	300
CEF94-PP	.....V.....H.....V.....N.....T.....L.....L.....N	300
D6948-PP	.....I.....Q.....I.....D.....A.....M.....I.....S	300
TY89-PP	.....	
Consensus	ITQPIYSIKL KIVTSKSGQQ AGDQMSMA. GSLAVTINGQ NYGALRPVT LVAYERVATO SVTVAGVEN FELIP	375
CEF94-PP	.....R.....	375
D6948-PP	.....S.....	375
TY89-PP	.....	
Consensus	WFLAURIVT EYGRFDGAM HTYLILSR DRIGIKTVWF TRSTIDWREY FMEVADLMSF LKINGAPGFK DIIRA	450
CEF94-PP	.....	450
D6948-PP	.....	450
TY89-PP	.....	
Consensus	.KRIAVPVVS TLPPAAFLA HAIGSDVYL LGDEAQAASQ TAAASQEAR AASGRIRGLT LAANDQYEVV ANLFO	525
CEF94-PP	I.....	525
D6948-PP	L.....	525
TY89-PP	.....	
Consensus	VPGPVVDGI LASFG.LGA HMLCVLRQ ATLPFVVITV VEDANTKAL HSKMFVING VEHLPQPSQ RGSVI	600
CEF94-PP	.....V.....	600
D6948-PP	.....I.....	600
TY89-PP	.....	
Consensus	RTLGRNVYO YAPQGVLSL TGRDITVVI DVWQDSIEL SKDPIPTVIG HSGHLAIAYV DVFRKVPIN VMTQ	675
CEF94-PP	.....	675
D6948-PP	.....	675
TY89-PP	.....	
Consensus	ALMA.GEIR. VSFRTSLAT ANKLGLALAG PGAFDVWTO. HRTTIRKVF HMPEDWOLF YLMLPLFPW AGROY	750
CEF94-PP	....C....K.....F.....	750
D6948-PP	....Y....N.....S.....	750
TY89-PP	.....T....P	28
Consensus	HLAMAASEFK RYFLESAVA AMEAAANVDP LPQSALSVPM MLEMGIVTD MANVALSDW AMGGNPLAN APQAG	825
CEF94-PP	.....	825
D6948-PP	D.....	825
TY89-PP	...L.....D.....D.....R...Q...K.....	103
Consensus	SKSQRAKYGT AGYQVEARGF TPKEAQREK. TRISKRETH GIYFATPWV ALNGHGPSP GGLKYNQWR KIPD	900
CEF94-PP	.....	900
D6948-PP	.....	900
TY89-PP	.....E.....	178
Consensus	NEDYLDVHA EKERLASSEQ ILRANTSIG APQARPPQA FIDEVAKVYE IIRKROPKQZ QMKLLATAM ENKRR	975
CEF94-PP	.....	975
D6948-PP	.....	975
TY89-PP	...F.....V.....R.....	253
Consensus	NFRAPPKK PKNAPTQVF PGLGHWIRT VSDQDL	1012
CEF94-PP	....L.....	1012
D6948-PP	.....A.....	1012
TY89-PP	.....S.....	290

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Fig.3b IBDV VP1 alignment

Consensus	MSD.FMSQA RS.IGAAPGI KPEAGQDVE LLIFKVVVF EDPLASTVEL AKFLAKMTE .LQFSLPFI EHYET	75
CEP94-VP1	...I.....T.....V.....	75
D6948-VP1	...V.....K.....I.....	75
Consensus	DQILPDLANI RQISGAVLKP TSLPFDQDS YPFKTYPTK PSKEKFWAYP FQIALAQKI TLFLQVFA. ...LKD	150
CEP94-VP1	.....N SD...	150
D6948-VP1	.....T EN...	150
Consensus	EVTLLTQNIH DKAYSGQYTH QGATKLVAKK EVATGQWPK DPLALQYTF SIAGLIDITL FVGPFGEDK FVVFL	225
CEP94-VP1	.....	225
D6948-VP1	.....	225
Consensus	TRVFERNLVL TGVVDG.FEV EDYLPKILK RSGSLTYGR THGTIGENI AISKQFLAKL S.LLQQAQT KQNK	300
CEP94-VP1	.....D.....T.....	300
D6948-VP1	.....E.....A.....	300
Consensus	IKLLSELSY WYLSQGLLP KARYDKSTW LKSTYHWEA PSPHKLHLM ITWFWHSEF HVLNIEGCT SLYTF	375
CEP94-VP1	.....	375
D6948-VP1	.....	375
Consensus	HPFAGLKEI VEMI.AP.EF KALVADNIT IVHENTWYSI DLKQENACT RQHQQAATY ILTHQKMDG DFWF	450
CEP94-VP1	.....L..E.....	450
D6948-VP1	.....N..D.....	450
Consensus	QTWATFANKI APALVVDSC LDESLQIKTY QGSGQAATY DSHLLSTLV LQQAEL.QP .FQSEVKEI EKLK	525
CEP94-VP1	.....R..R.....	525
D6948-VP1	.....K..S.....	525
Consensus	INPIERSID DIERKLAQLV .LAQFOYLG QVEFEQ.SPT VELDLQWHA TTKULQITV FVLCKELFC SAAYP	600
CEP94-VP1	.....L.....S.....	600
D6948-VP1	.....P.....P.....	600
Consensus	KGVKSKLS KVICQATKV VRYEALRLVG GNTYPLHKA CQMA.AAKR HLEAGGFYLD EYLSKELS EFGZA	675
CEP94-VP1	.....G.....	675
D6948-VP1	.....S.....	675
Consensus	FEGPHILTV T.ESLAKLS. PVPPKPPVVM RFWYTGGLA VSHALQYRY KIRAGLSGLV LIATARSLO DAVKA	750
CEP94-VP1	.....S.....K.....	750
D6948-VP1	.....P.....R.....	750
Consensus	KAAKILSKS KPDQPDAMP ERSETLSLL EKADIASKVA HVALVETSDA LEAVQSTSVY THCTPEVKNP QTASH	825
CEP94-VP1	.....	825
D6948-VP1	.....	825
Consensus	FVGHKLPK RATGVQALL GASTSRPKK EAPTSKNAV KMAKIQCK ESQ..	881
CEP94-VP1	.....QF	881
D6948-VP1	.....	879

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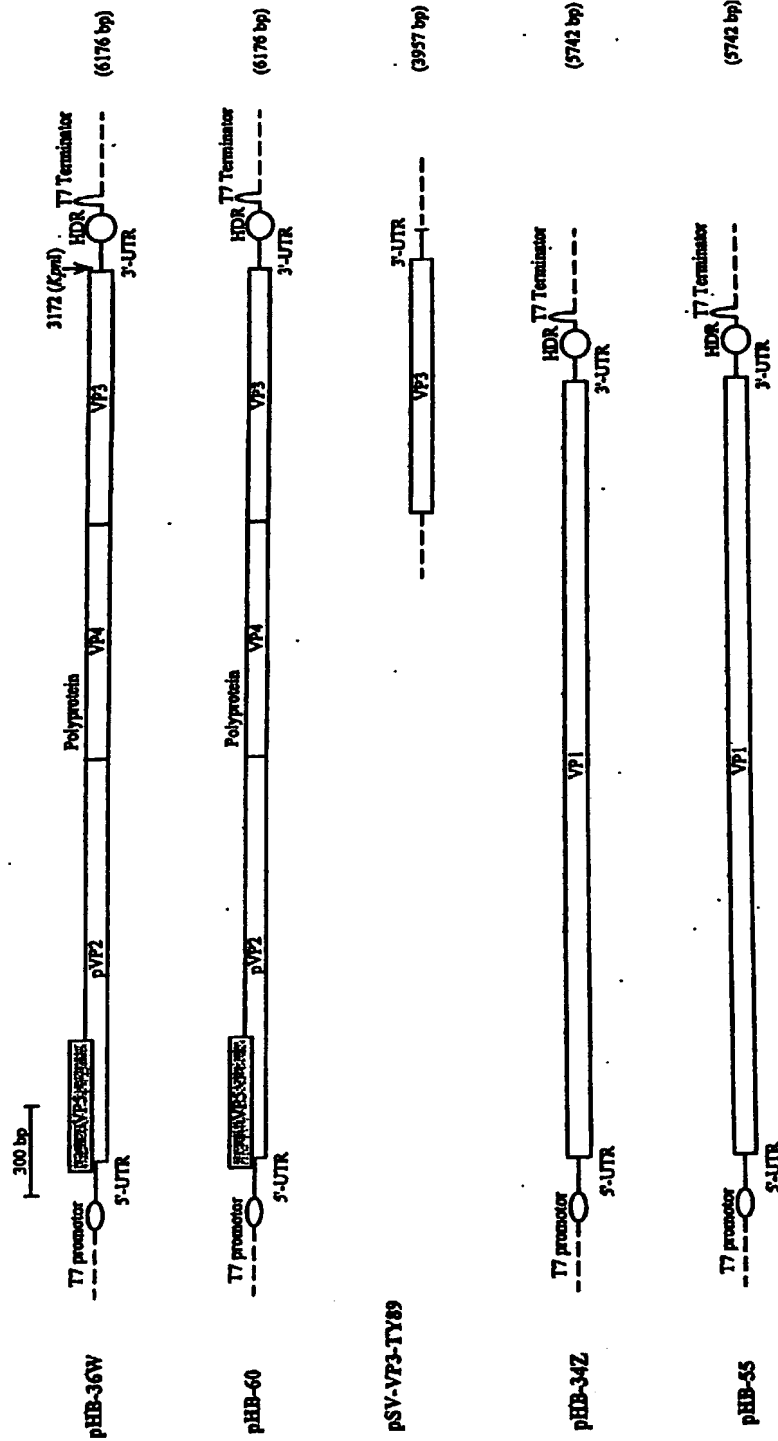
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Fig. 3c IBDV VP5 alignment.

Consensus	MVSRDQINER SDD.PARSHF TDCSVHTFSS DANRRTGVNS GRHP.EANSQ	50
D6948-VP5	.....E.....R.....	50
CEF94-VP5	.....K.....G.....	50
Consensus	VRDLQLQFDC GGHRVRANCL FFW.FWLNCG CSLHFAQWE LQVRSDAPDC	100
D6948-VP5	.....F.....	100
CEF94-VP5	.....I.....	100
Consensus	PEPTQLQLL QASESESSE VIGT.WWRLC TK.HHQRDL FKKPE	145
D6948-VP5	.....F.....M.....	145
CEF94-VP5	.....S.....R.....	145

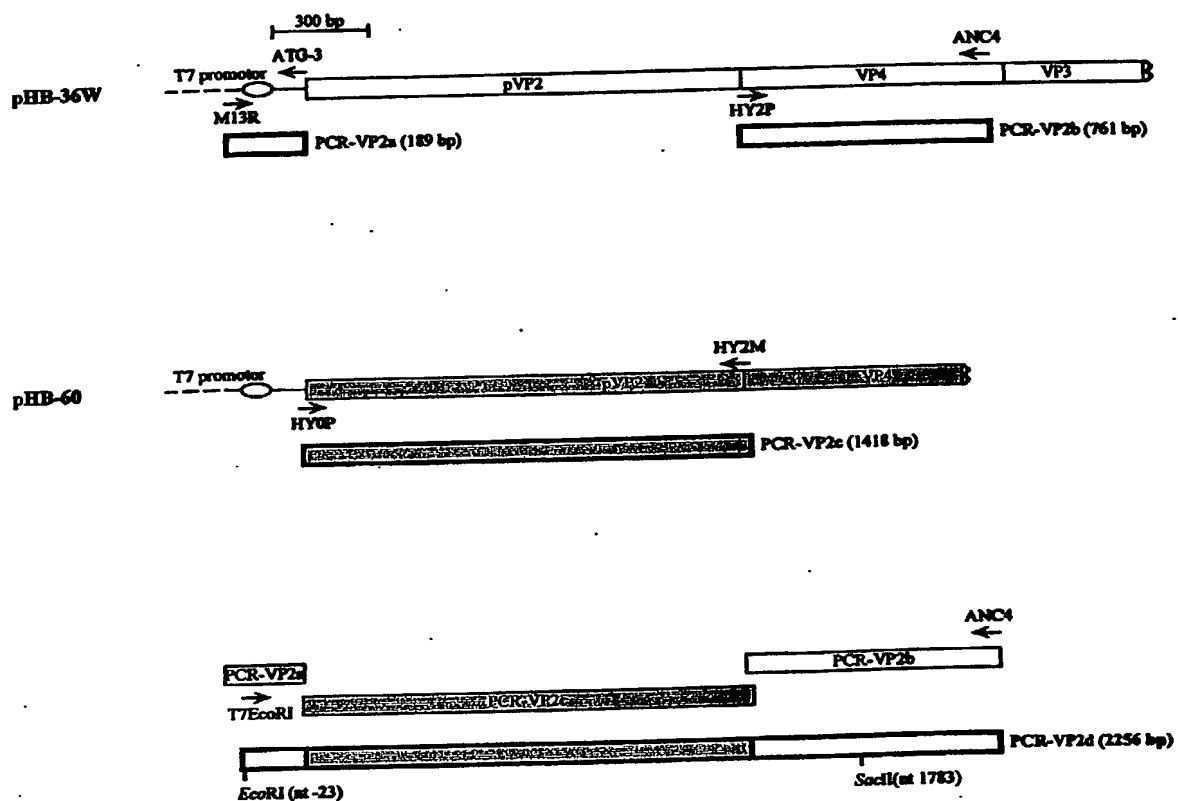
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Fig. 4 Schematic representation of the used plasmids



**Fig. 5a**

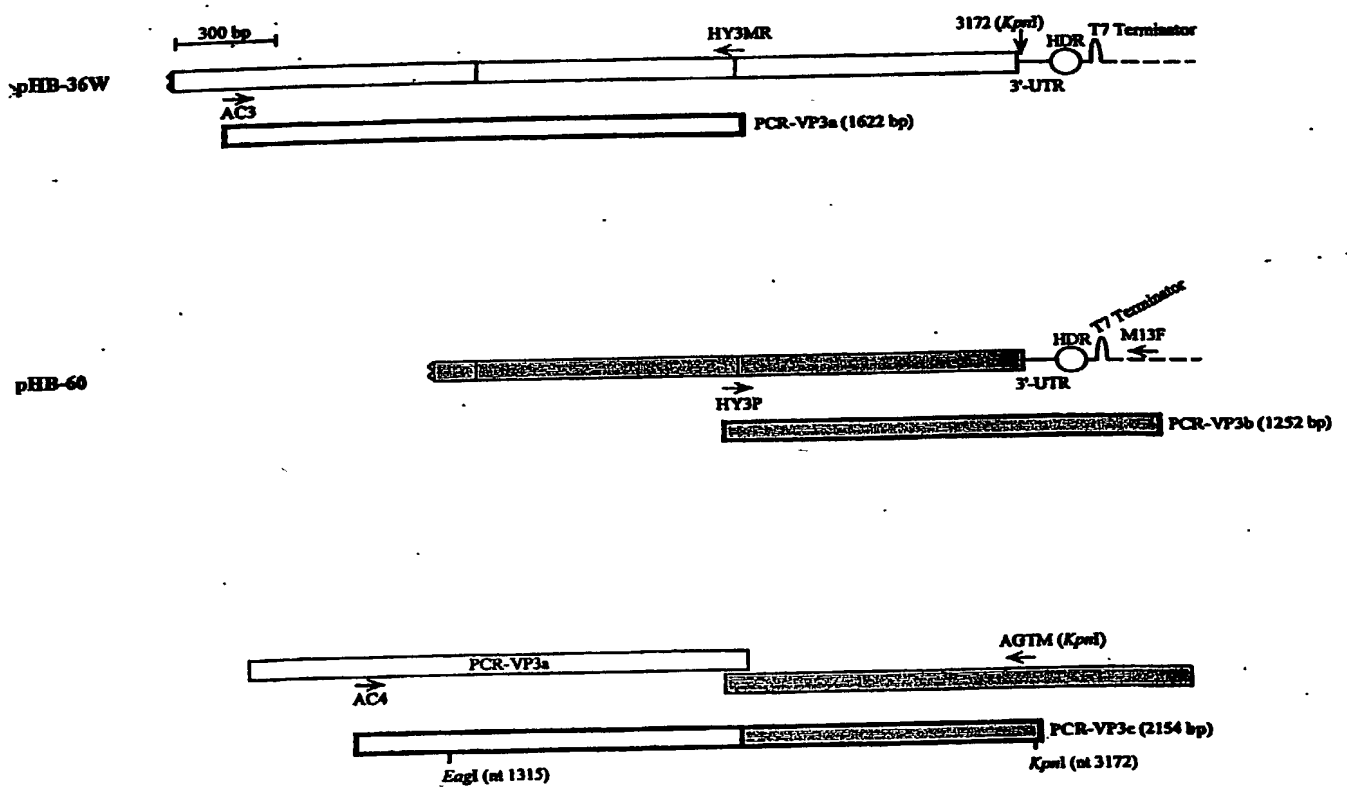
Schematic representation of the construction of PCR fragment PCR-VP2d



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**Fig. 5b** Schematic representation of the construction of PCR fragment PCR-VP3c

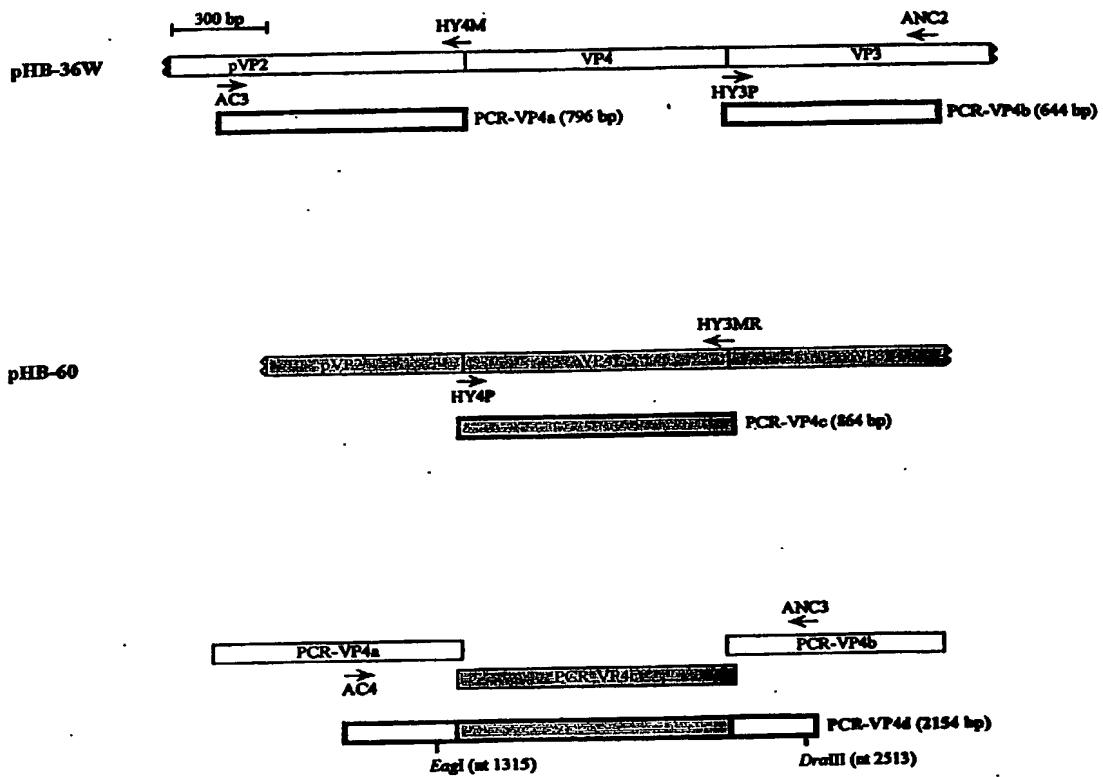


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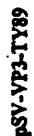
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**Fig. 5c**

Schematic representation of the construction of PCR fragment PCR-VP4d



**Fig. 5d**





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Fig. 5e Schematic representation of the construction of plasmid pHB36-ΔVP3C

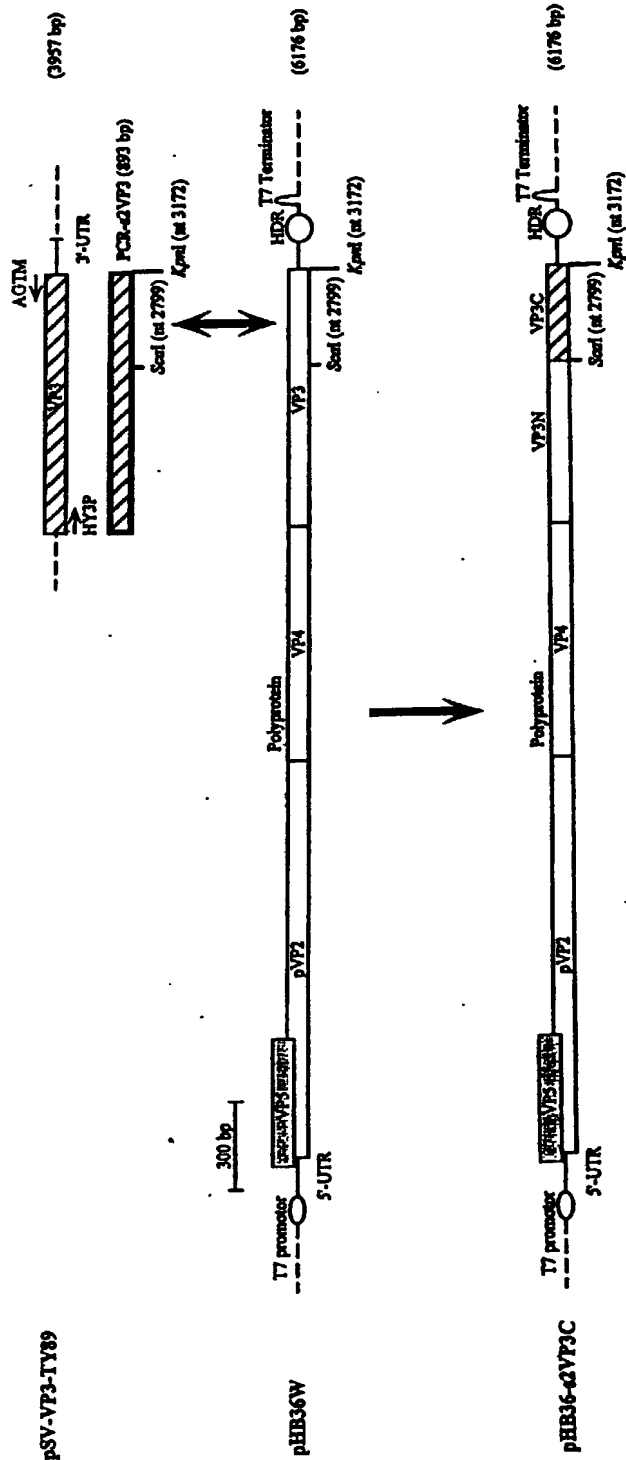
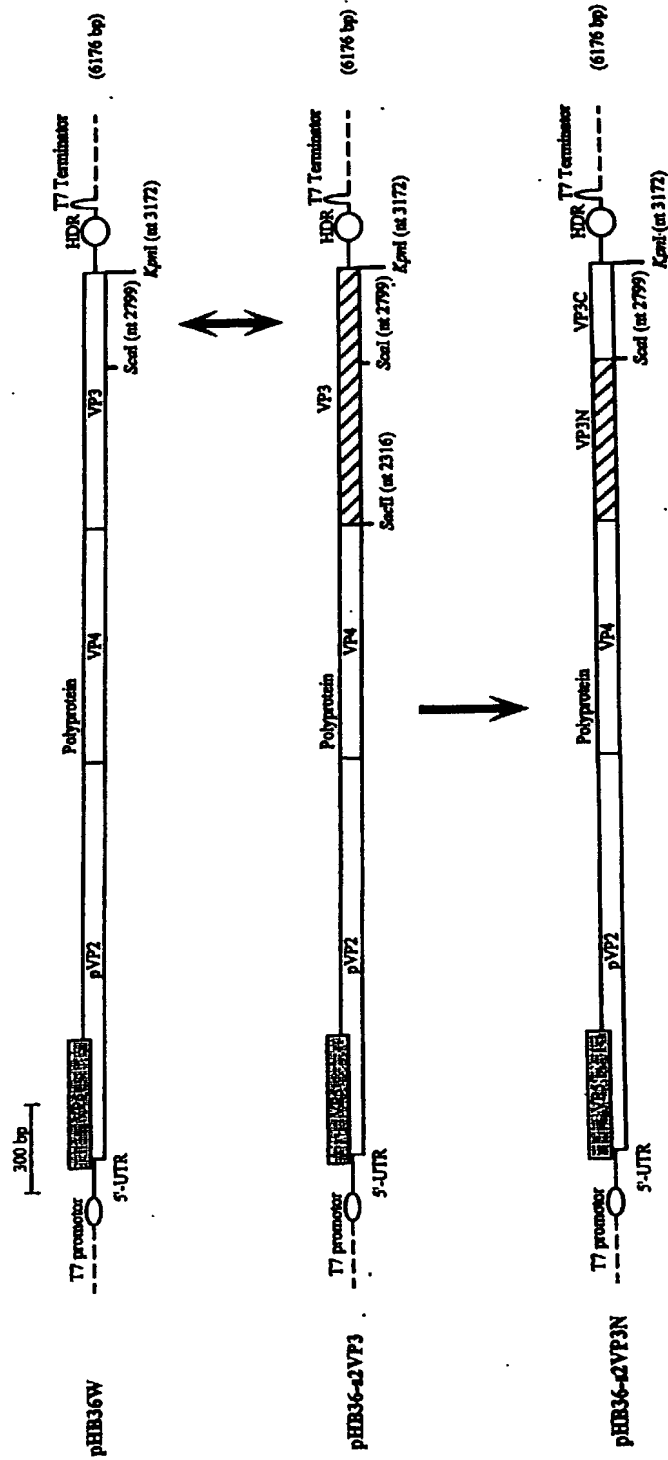
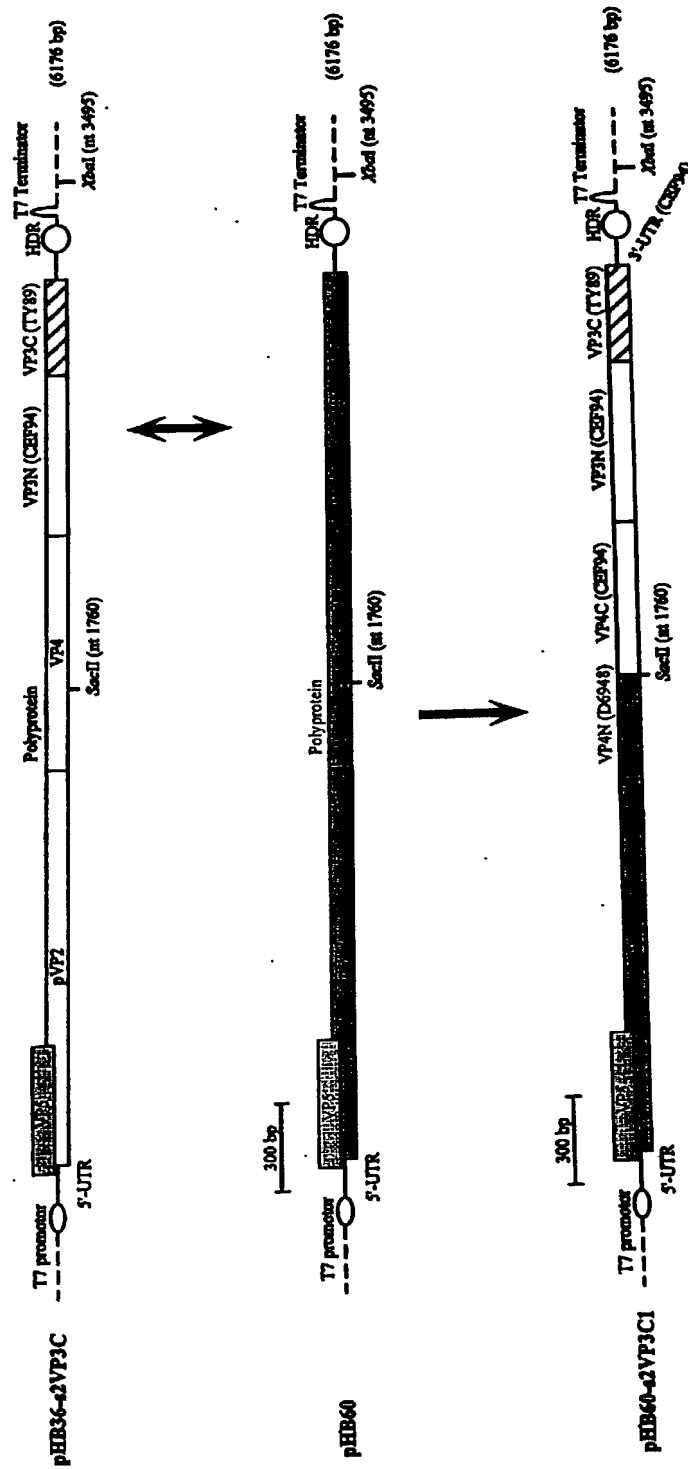


Fig. 5f Schematic representation of the construction of plasmid pHB36-Δ2VP3N



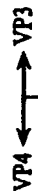
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Fig. 5g Schematic representation of the construction of plasmid pHB60-Δ2VP3C1



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Fig. 8C

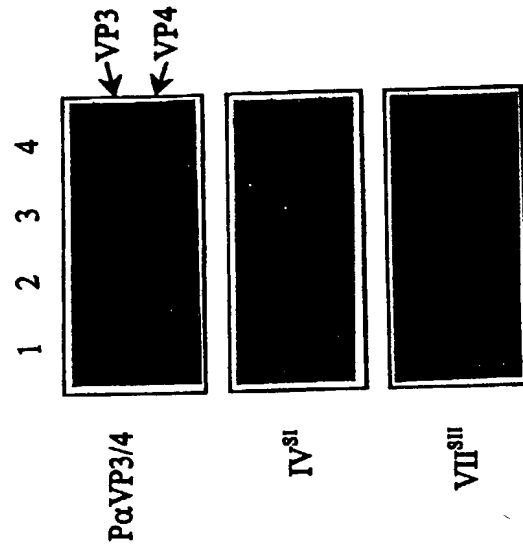


Fig. 8B

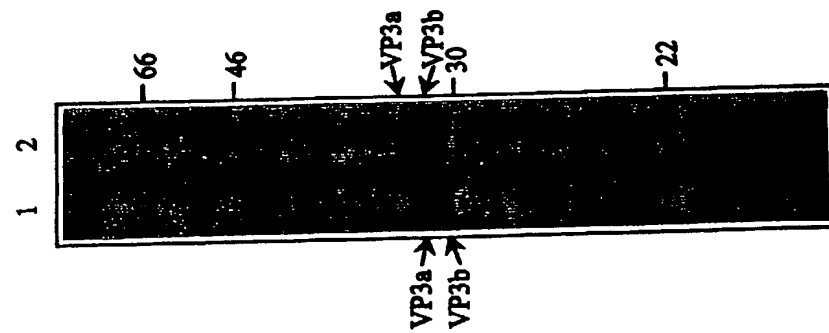
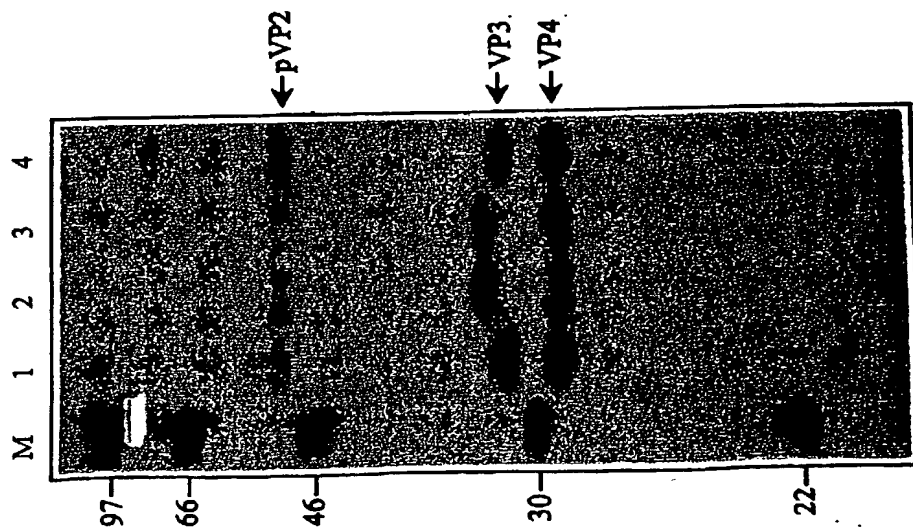


Fig. 8A



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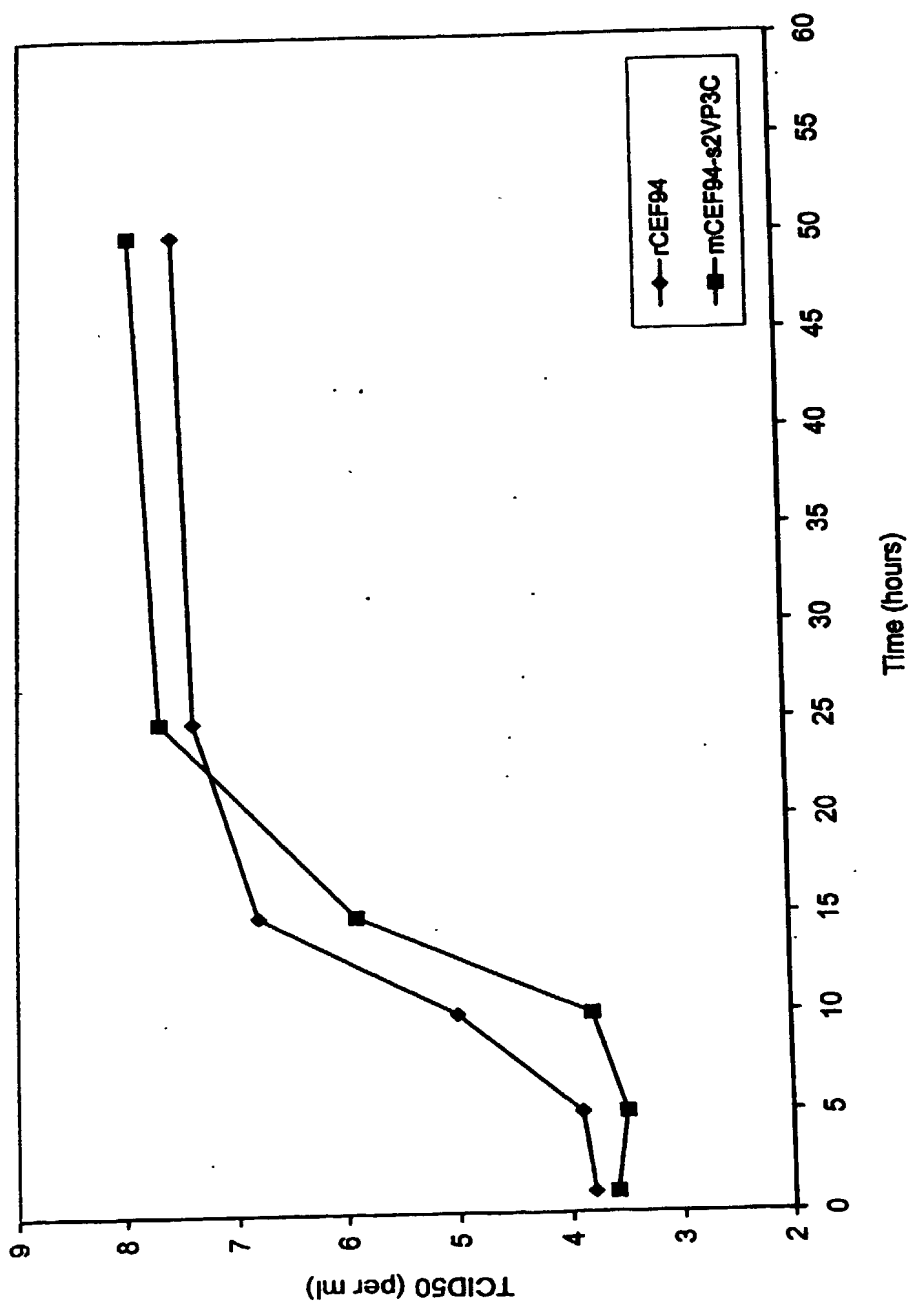
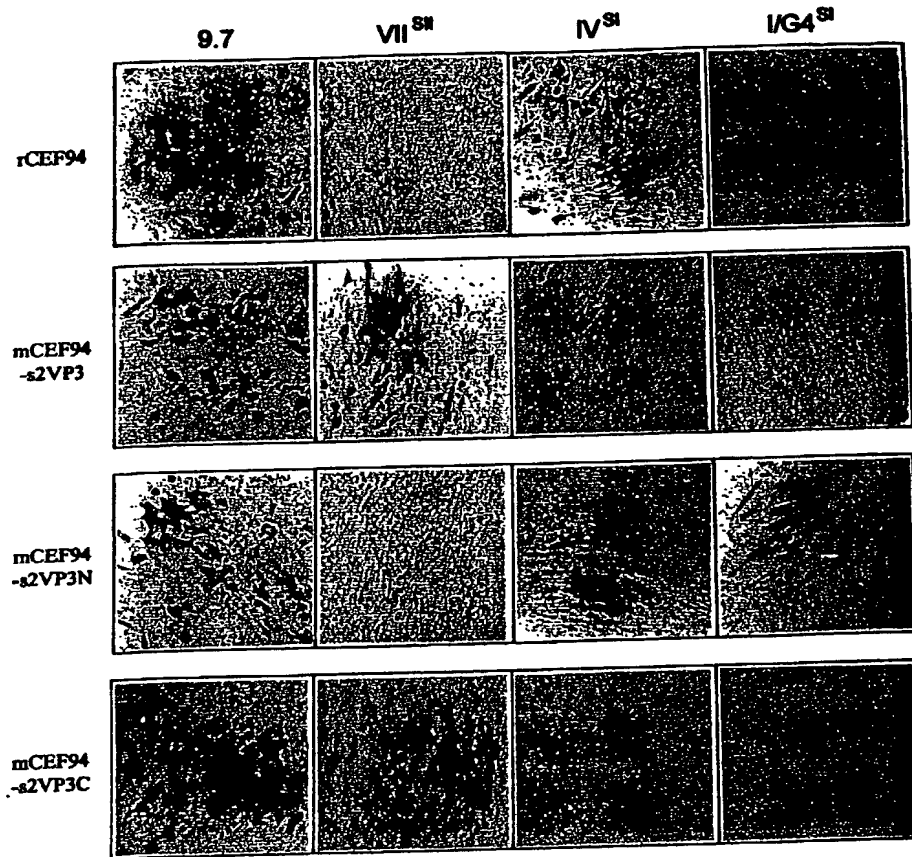


Fig. 9

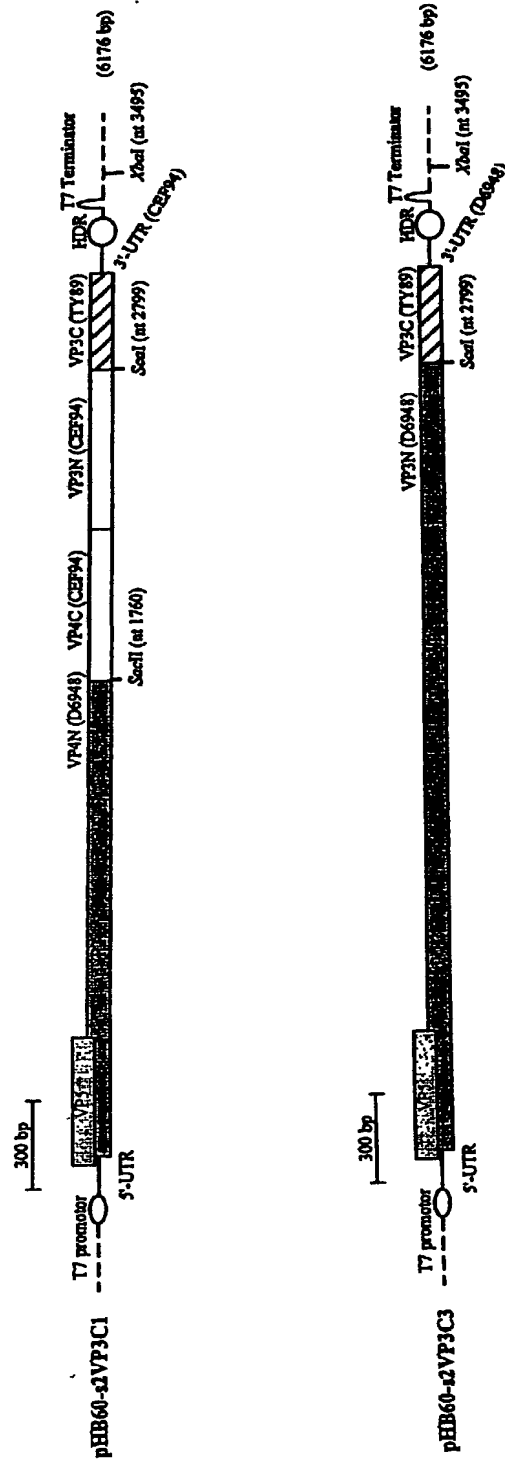
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Fig. 10





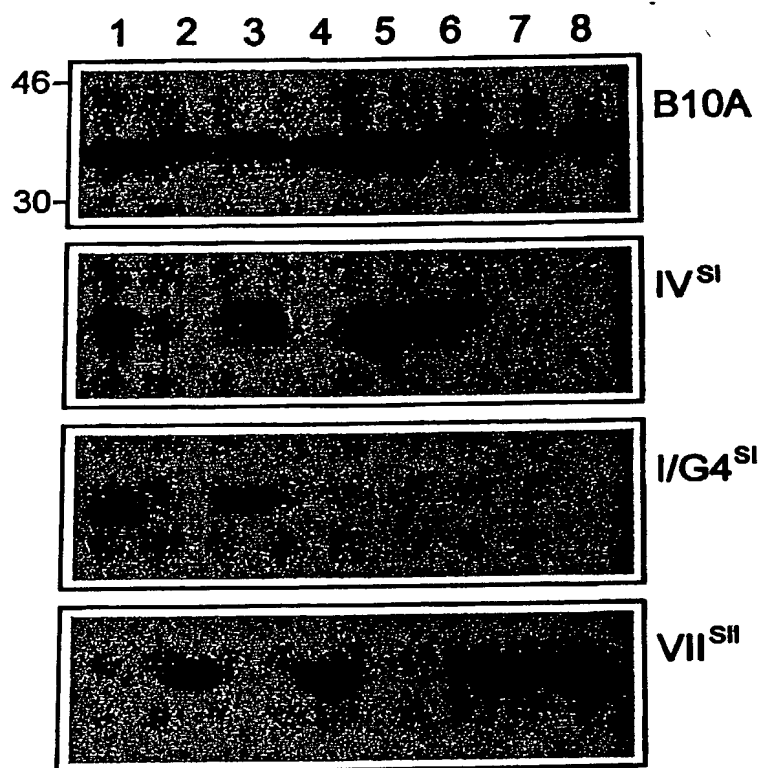
Schematic representation of plasmids pHB60-s2VP3C1 and pHB60-s2VP3C3



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**Fig. 12**



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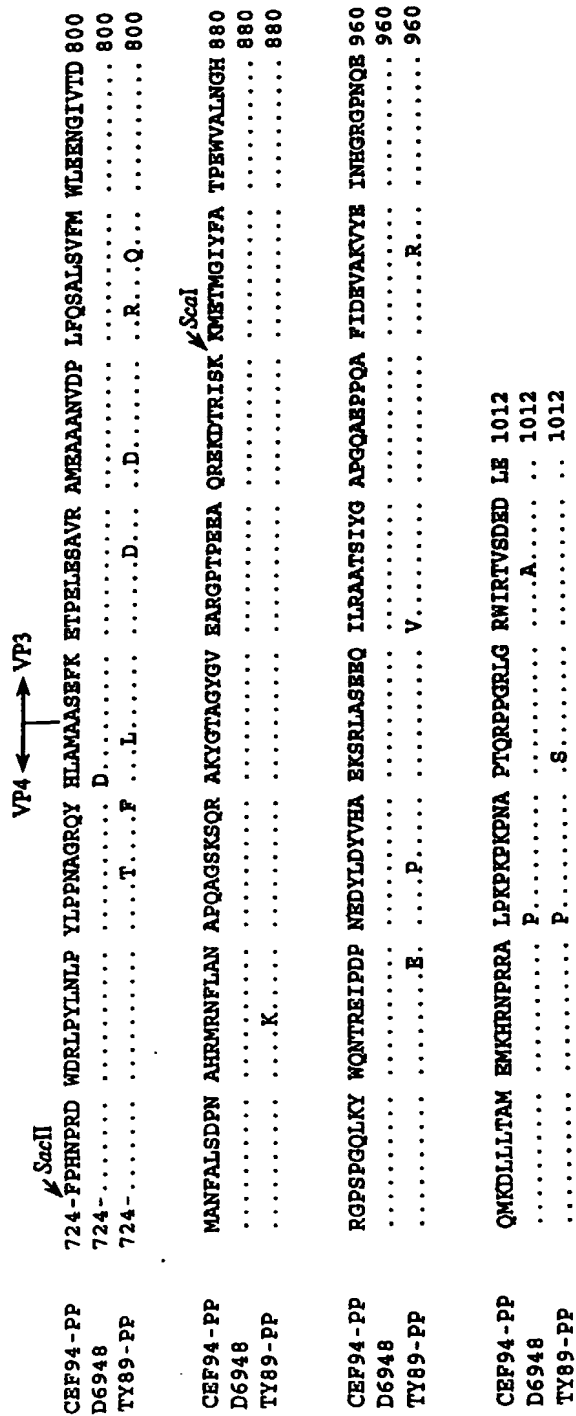
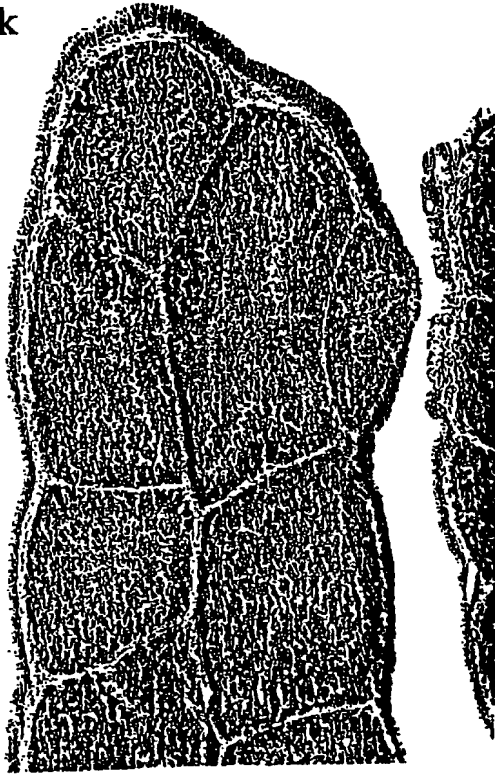


Fig. 14

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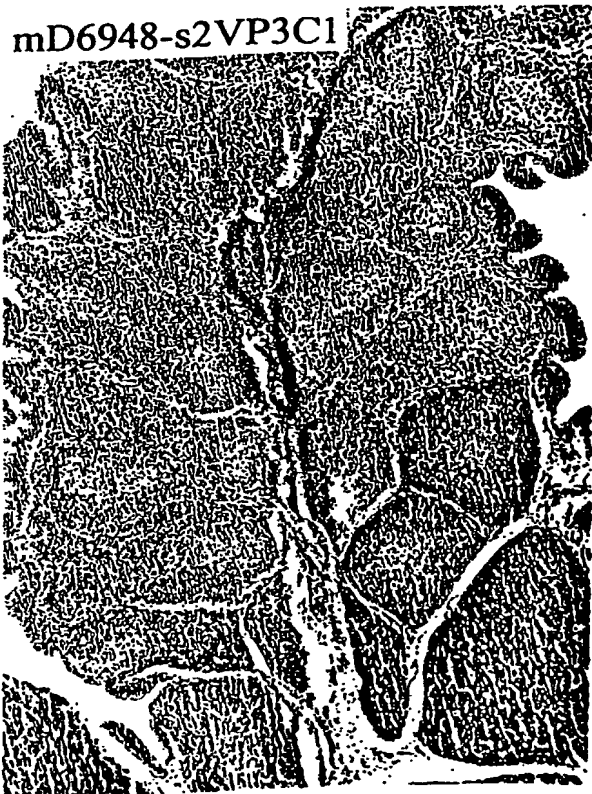
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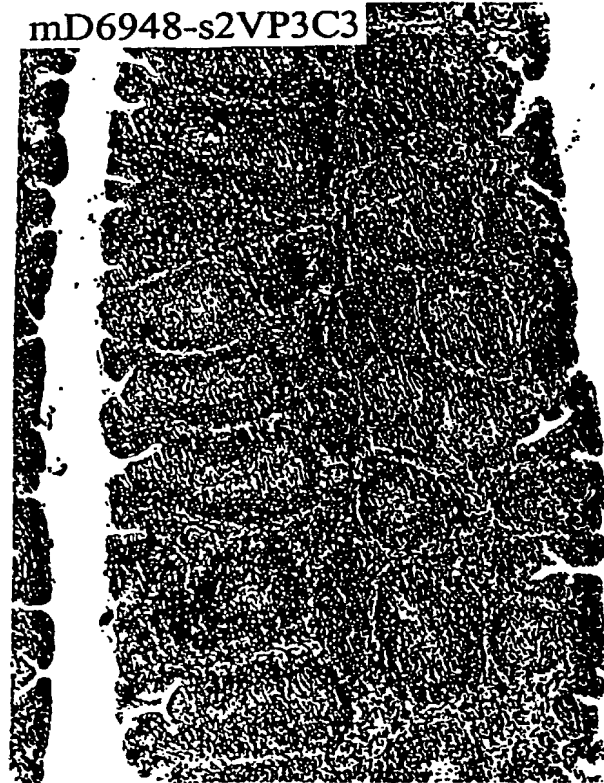
D6948



mD6948-s2VP3C1



mD6948-s2VP3C3

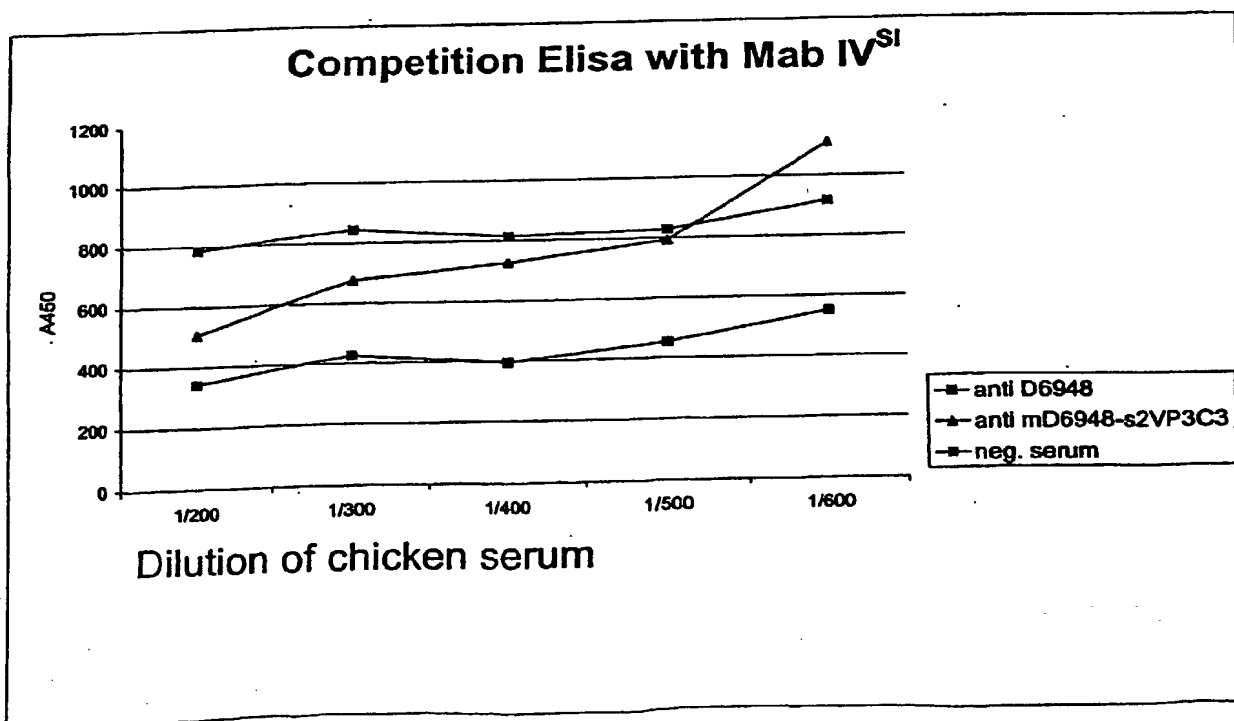
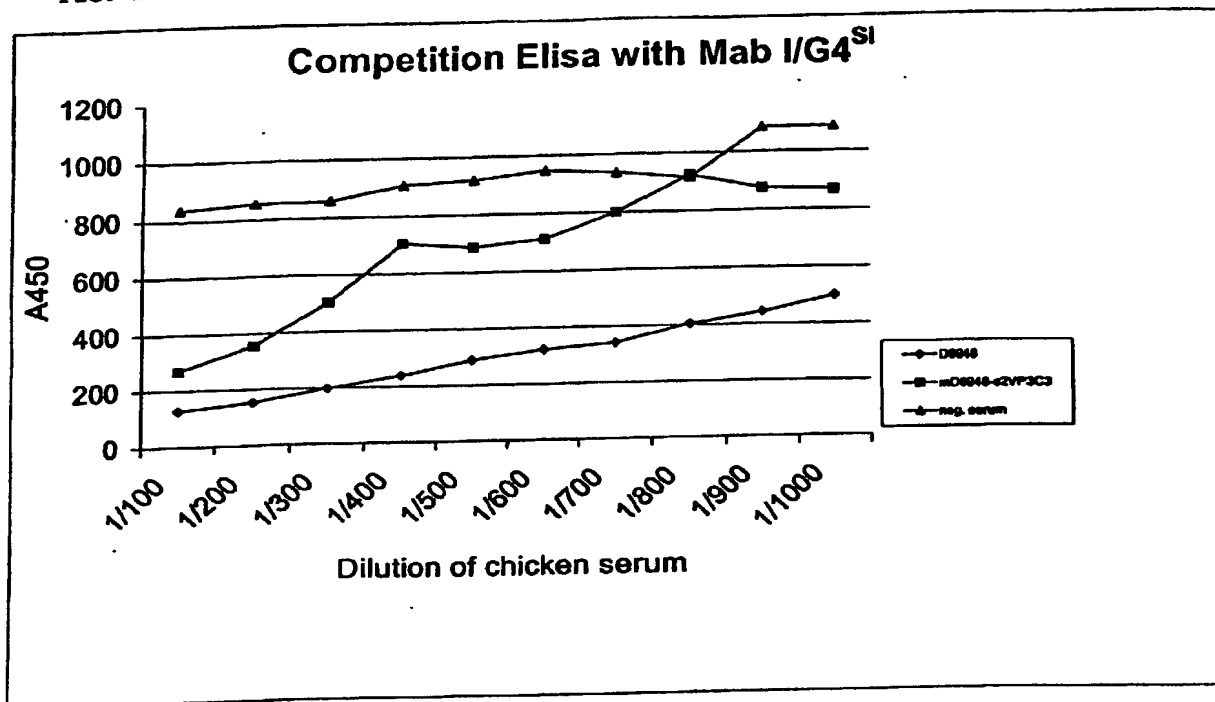


**TITLE: MOSAIC INFECTIOUS BURSAL  
DISEASE VIRUS VACCINES**

Inventor: Boot et al.  
Serial No.: 10/046,671  
Docket No.: 2183-5238US

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**FIG. 15**



TITLE: MOSAIC INFECTIOUS BURSAL  
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Fig. 16A

D6948-VP5	MLSLMVSRDQ	TNDRSDDEPA	RSNPTDCSVH	TEPSDANNRT	GVHSGRHPRE	AHSQVRDLDL	QFDCGHRVR	ANCLF	75
CEF94-VP5	-----	K			G				71
	PWFPLNCGC	SLHTAEQWEL	QVRSDAPDCP	EPTGQLQLLQ	ASESESHSEV	KHTPWRLCT	KNEHKRDLP	RKPE	149
	I			S		R			145

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Fig. 16B

D6948-PP MTNLQDQTQQ IVPFIRSLIM PTTGPASIPD DTLEKHTLRS ETSTYNLTVG DTGSGLIYFF PGPPGSIYGA HYTLQ 75  
CEF94-PP SNGNYKFDQM LLTAQNLPAS YNYCRLVRS LTVRSSTLPG GUYALNGTIN AVTFQGSLSLSE LTDVSYNGLM SATAN 150  
INDKIGNVLV GEGVTVLSP TSYDLGVRL GDPIPAIGLD PKMVATCDSS DRPRVYTITA ADDYQFSSQY QAGGV 225  
TITLFSANID AITSLSIGGE LVFQTSVQGL ILGATIIYIG FCGTAVITRA VAADNGLTAG TDNLMPFNIV IPTSE 300  
ITQPITSIKL EIVTSKSGGQ AGDQMSWSAS GSLAVTIHGG NYPGALRPVT LVAYERVATG SVTVVAGVSN FELIP 375  
NPBLAKNLVT EYGRFDPGAM NYTKLILSER DRIGIKTVMP TREYTDREY FMEVADLNSP LKIAGAFGFK DIIRA 450  
LRRJAVPVVS TLPPPAAPLA HAIGEGVDYL LGDEAORASG TARASGKAR AASGRIROLT LAADKGYEVV ANLEQ 525  
VPONPVADGI LASEPGILRGA HNLCVLREG ATLEFVILTT VEDAMTKAL NKKMEAVIEG VREDLORPESQ RGSFI 600  
RTLSGHRVYG YAPDGVLPDE TGRDYTVVPL DDVMDDSIML SKOPIPIVNG NSGNLATAYM DYFRPKVPIH VAMTG 675  
ALNAYGEIEN VSRSTKLAT AHRIGLKLAG EGAEDVNTGS NWATEIKRPP ENPRDMDRLP YLNLPLYLPN AGROY 750  
DLAMAASEFK ETPELESVR AMEAAANVDP LFQSALSVM WLENGIYTD MANTALSDFN AHRMNFILAN APQAG 825  
SKSQRAKYGT AGYGVREARCP TPPEAQREKD TRISKMETM GIYFATPEWV ALNGHRGPSP GOLKYWONTR EIPDP 900  
NEDYLDYVHA EKSRLASEEQ ILRAATSIYG APQAEPPQA FIDEVAKYVE INHGRGPQOE QMKDILLITAM EMKHR 975  
NPRRAPPKPK PKVNAPTQRP PGRIGRWIRA VSEDELE 1012  
L T

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Fig. 16C

D6948 -VP1  
CEP94 -VP1

MSDVNSPQA RSKISAAGI KFTAGQDVEE LLIPKVVVPP EDPLASPSRL AKFLRENGYK ILQPSRLPEN BEYET 75  
I T V  
DQILPDLAWM RQIEGAVLKP TILSLPIGDQE YFPKYVPTHR PSKEKNAYP PDIALLKQMI YLFLQVPEAT DNLKD 150  
N EQ  
EVTLLTQNR DKAYSGTYM GQATRLVAMK EVATGRPNK DPLKLGTYFE SIAQLDITL PVGPPGQDDX PNVPL 225  
TRVPSRMLVL TGDVDGEFEV EDYLPKINLK SSSGLPVVGR TKGETIGEMI AISNQFLREL SALLKQDAGT KGSNK 300  
D T  
KKLLSMLSDY WYLSGGLLFP KAERYDKSTM LTKTRNIWSA PSPTHLMISM ITWPMNSNP NNVLNIEGCP SLYKF 375  
NPPRGGILNRI VENIMAPDEP KALVYADNIY IVHSNTWYSI DLEKGEANCT RQENQAAMYI ILTRGWSNDG DPMFN 450  
L E  
QTWATFAMNI APALVVDSSC LIMNLQIKTY GQSGNAATF INNELLSTLV LDQNNLMKQP SPDSEEFKSI EDKLG 525  
R R  
INFKIERID DIRGKLRQLV PLAQPGYLSG GVEPEQPSEPT VELDLGWSA TYSKDLGIYV PVLDKERLFC SAAYP 600  
L S  
KGVENKSLKS KVGIEQAYKV VRYEALRLVG GMYPLANKA CKNNASAARR HLEAKGFPLD EFLAENSELS EFOEA 675  
G  
FEGFNKLTV TPESLAELNR PVPPKPPNVN RPVNTGGLKA VSNALKTGRY RNEAGLSGLV LLATARSRLQ DAVKA 750  
S K  
KAAEKLHKS KPDDPDADWF ERSETLSDLL EKADIASKVA HSALVETSDA LEAVQSTSVY TPKYPEVKNP QTASN 825  
PVGGLHLPK RATGVQAALL GAGTERPMGM EAPTRSKNAV KAAKRRQRQK ESRQ-- 879  
QP 881



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Fig. 17

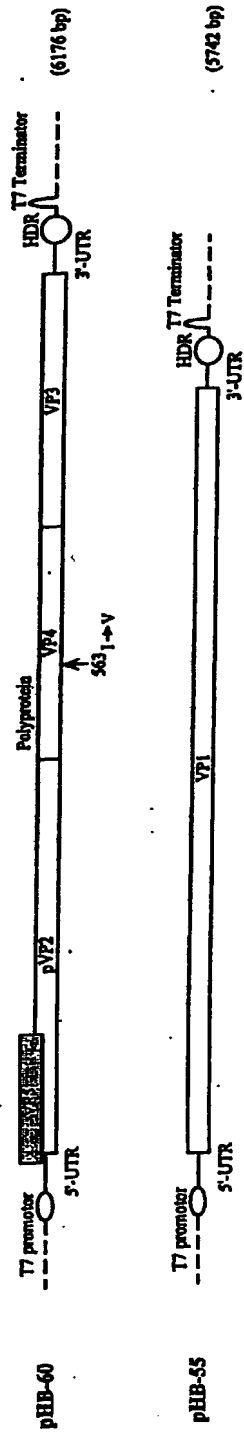


Fig. 18c

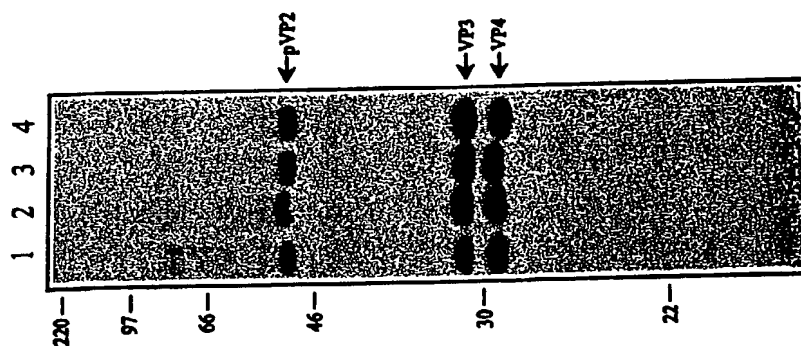


Fig 18b

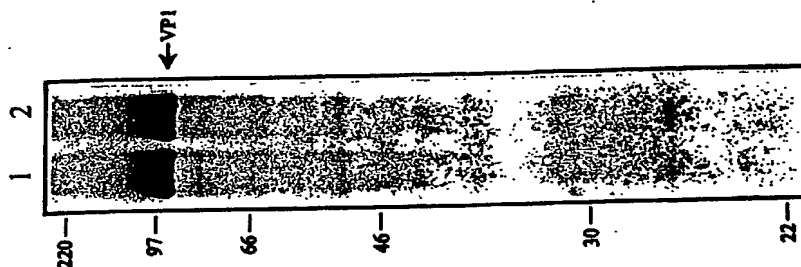
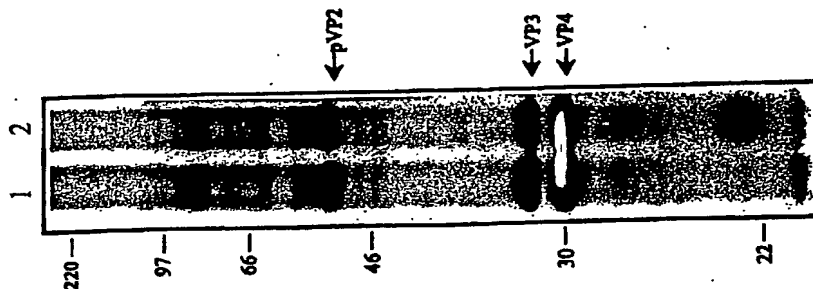
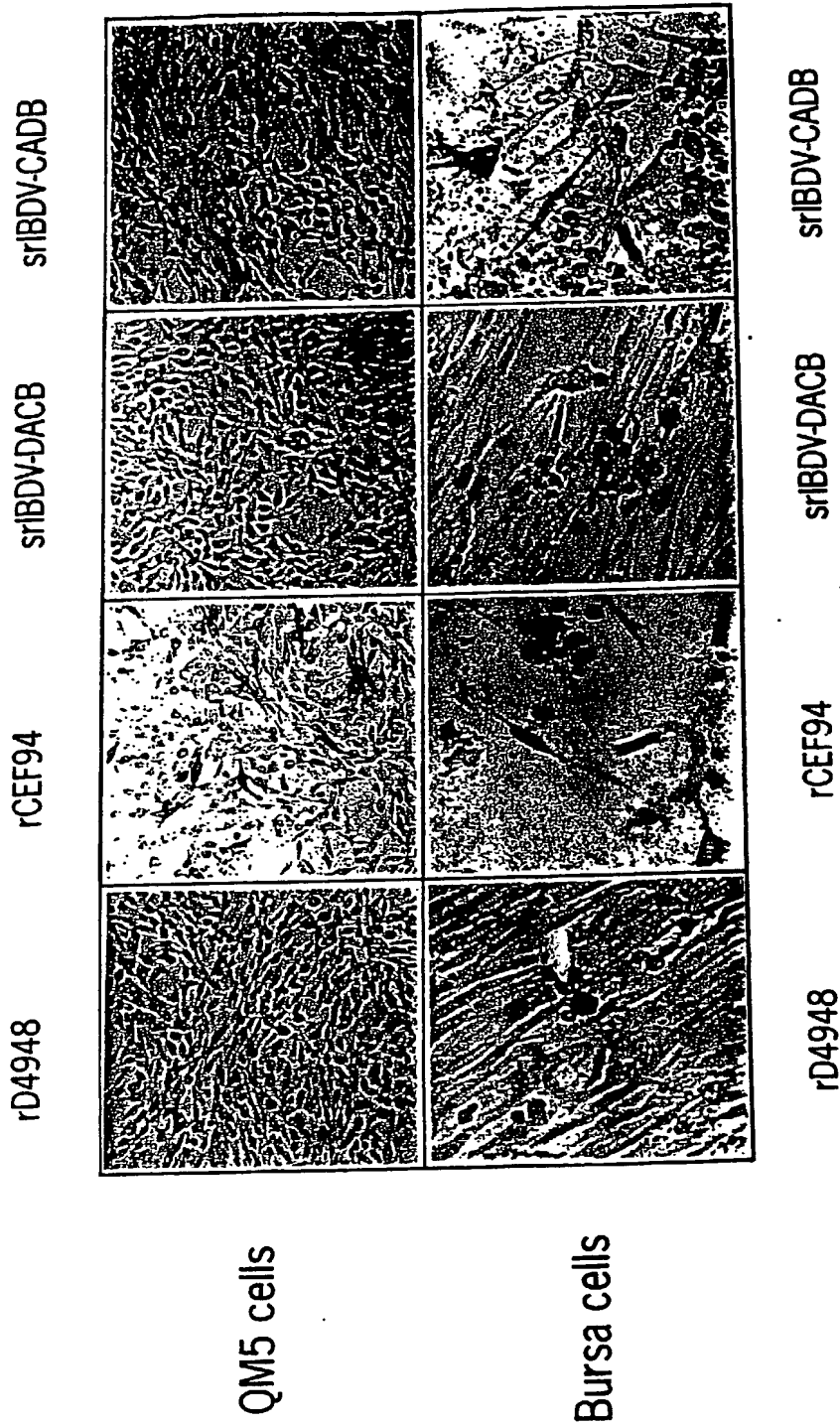


Fig. 18a



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Fig. 19



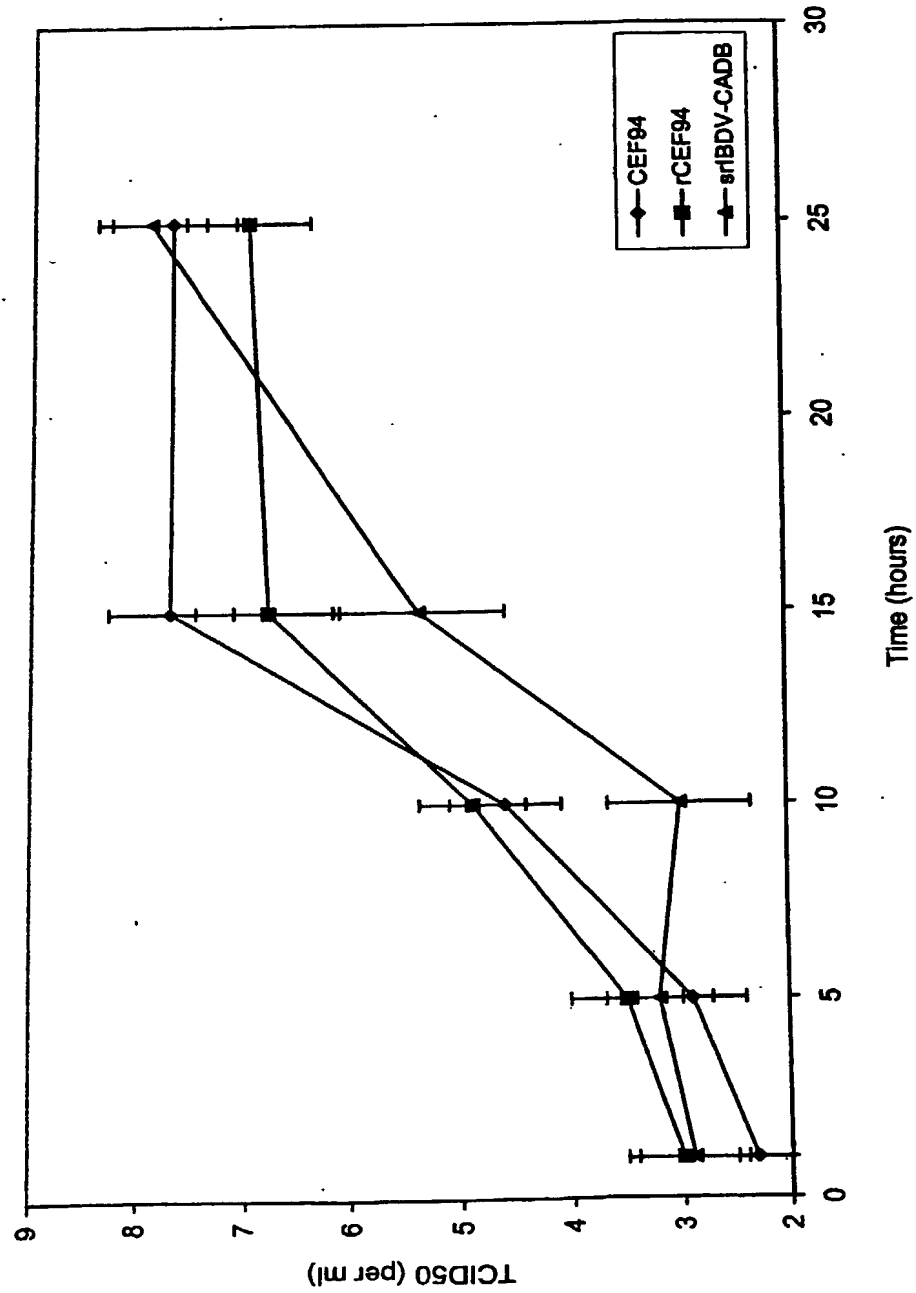


Fig. 20

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Fig. 21

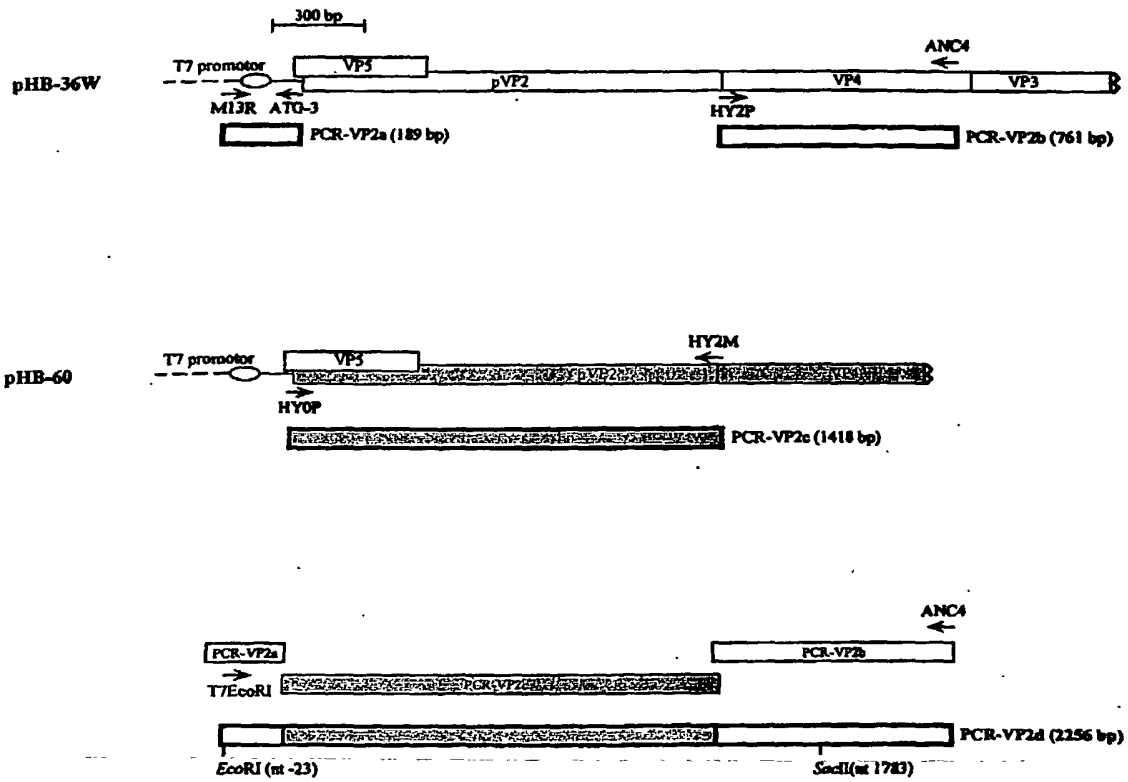


Fig. 22

